

FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 50.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LRGG 6
|||
Db 8 LRGG 11

RESULT 4

Q8UT17

ID Q8UT17 PRELIMINARY; PRT; 14 AA.
AC Q8UT17;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein.
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00BW2127.214;
RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RT "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
RT vaccine design.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF443105; AAL34832.1; -.
SQ SEQUENCE 14 AA; 1486 MW; 1F8F11F22AA03E20 CRC64;

Query Match 50.0%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LRGG 6
|||
Db 8 LRGG 11

RESULT 5

Q9QVJ3

ID Q9QVJ3 PRELIMINARY; PRT; 18 AA.
AC Q9QVJ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carbonic anhydrase-III, CA III (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92017893; PubMed=1922100;
 RA Stanton L.W., Ponte P.A., Coleman R.T., Snyder M.A.;
 RT "Expression of CA III in rodent models of obesity."
 RL Mol. Endocrinol. 5:860-866(1991).
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2077 MW; D12DF77457FD40F8 CRC64;

Query Match 50.0%; Score 4; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LRGG 6
 ||||
 Db 1 LRGG 4

RESULT 6

Q9UR83

ID Q9UR83 PRELIMINARY; PRT; 19 AA.
 AC Q9UR83;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Alcohol acetyltransferase (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94122444; PubMed=7764365;
 RA Minetoki T., Bogaki T., Iwamatsu A., Fujii T., Hamachi M.;
 RL Biosci. Biotechnol. Biochem. 57:2094-2098(1993).
 SQ SEQUENCE 19 AA; 2155 MW; F3562C9A57F6720A CRC64;

Query Match 50.0%; Score 4; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RGGR 7
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 Db 2 RGGR 5

RESULT 7

Q8IU87

ID Q8IU87 PRELIMINARY; PRT; 19 AA.
 AC Q8IU87;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein S (Fragment).
 GN PROS1.

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hamasaki N., Dong Chon K., Kinoshita, S, Iida H., Inoue S.,
RA   Watanabe K., Kurihara M., Wada Y., Ono M.;
RT   "Gene analysis of anticogulation factors in Japanese thrombotic
RT   patients. Genetic background of thrombophilia in Japan.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB083392; BAC54140.1; -.
DR   EMBL; AB083395; BAC54143.1; -.
DR   EMBL; AB083396; BAC54144.1; -.
FT   NON_TER      19      19
SQ   SEQUENCE     19 AA;  1972 MW;  708616BFDFE37112 CRC64;

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Query Match          50.0%;  Score 4;  DB 4;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 9.1e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      5 GGRC 8
        ||||
Db      5 GGRC 8

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RESULT 8

Q8NET0

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ID   Q8NET0          PRELIMINARY;          PRT;      21 AA.
AC   Q8NET0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Defensin beta 112 (Fragment).
GN   DEFB112.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21843921; PubMed=11854508;
RA   Schutte B.C., Mitros J.P., Bartlett J.A., Walters J.D., Jia H.P.,
RA   Welsh M.J., Casavant T.L., McCray P.B. Jr.;
RT   "Discovery of five conserved beta-defensin gene clusters using a
RT   computational search strategy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:2129-2133(2002).
DR   EMBL; AY122469; AAM93911.1; -.
DR   Genew; HGNC:18093; DEFB112.
FT   NON_TER      1      1
FT   NON_TER      21     21
SQ   SEQUENCE     21 AA;  2290 MW;  2680D6A5265BE766 CRC64;

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Query Match          50.0%;  Score 4;  DB 4;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 9.8e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy 5 GGRC 8
 ||||
Db 6 GGRC 9

RESULT 9

Q9U5M8

ID Q9U5M8 PRELIMINARY; PRT; 21 AA.
AC Q9U5M8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Sex-lethal orthologous protein (Fragment).
GN SXL.
OS Megaselia scalaris.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Platypezoidea; Phoridae; Megaseliini; Megaselia.
OX NCBI_TaxID=36166;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wien;
RA Sievert V., Kuhn S., Paululat A., Traut W.;
RT "Sequence conservation and expression of the Sex-lethal homologue in
RT the fly Megaselia scalaris."
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X98770; CAB61830.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2373 MW; FE7A60CF03FC0319 CRC64;

Query Match 50.0%; Score 4; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RGGR 7
 ||||
Db 3 RGGR 6

RESULT 10

Q63480

ID Q63480 PRELIMINARY; PRT; 7 AA.
AC Q63480;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;

RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
DR EMBL; U59125; AAB02827.1; -.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RGG 6
|||
Db 3 RGG 5

RESULT 11

O89965

ID O89965 PRELIMINARY; PRT; 8 AA.
AC O89965;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Agnoprotein (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98244352; PubMed=9584961;
RA Boldorini R., Caldarelli-Stefano R., Monga G., Zocchi M., Mediatì M.,
RA Tosoni A., Ferrante P.;
RT "PCR detection of JC virus DNA in the brain tissue of a 9-year-old
RT child with pleomorphic xanthoastrocytoma.";
RL J. Neurovirol. 4:242-245(1998).
DR EMBL; AF064547; AAC23995.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1002 MW; ED15B736C40732C6 CRC64;

Query Match 37.5%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4
|||
Db 2 VLR 4

RESULT 12

Q8R514

ID Q8R514 PRELIMINARY; PRT; 9 AA.
AC Q8R514;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Annexin II (Fragment).
 GN ANX2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ozeki M., Hoshino S., Hiai H., Toyokuni S.;
 RT "Identification and characterization of an annexin II pseudogene in
 RT rat.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB072615; BAB88856.1; -.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 896 MW; 893768786411B775 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RGG 6
 |||
 Db 5 RGG 7

RESULT 13

Q99JF4

ID Q99JF4 PRELIMINARY; PRT; 9 AA.
 AC Q99JF4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Oct-1L (Fragment).
 GN OCT-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pankratova E.V., Deyev I.E., Zhenilo S.V., Polanovsky O.L.;
 RT "Tissue-specific Oct-1 isoforms from murine lymphocytes.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ310124; CAC34946.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 998 MW; 540BCEBAB5BEBAA7 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVL 3
 |||
 Db 7 CVL 9

RESULT 14

Q9IBM8

ID Q9IBM8 PRELIMINARY; PRT; 9 AA.
AC Q9IBM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Papovavirus BK (Gardner derived clone BKV9) early transcription
DE control region (Fragment).
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=46771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gardner;
RX MEDLINE=87061221; PubMed=3023684;
RA Chuke W.F., Walker D.L., Peitzman L.B., Frisque R.J.;
RT "Construction and characterization of hybrid polyomavirus genomes.";
RL J. Virol. 60:960-971(1986).
DR EMBL; M14452; AAA96236.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1130 MW; C7FD15B736C40732 CRC64;

Query Match 37.5%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4
|||
Db 2 VLR 4

RESULT 15

Q9PYK1

ID Q9PYK1 PRELIMINARY; PRT; 9 AA.
AC Q9PYK1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Papovavirus BK (Gardner) early transcription control region
DE (Fragment).
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=46771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gardner;
RX MEDLINE=87061221; PubMed=3023684;
RA Chuke W.F., Walker D.L., Peitzman L.B., Frisque R.J.;
RT "Construction and characterization of hybrid polyomavirus genomes.";
RL J. Virol. 60:960-971(1986).
DR EMBL; M14451; AAA96235.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1130 MW; C7FD15B736C40732 CRC64;

Query Match 37.5%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4
|||
Db 2 VLR 4

Search completed: November 13, 2003, 10:38:11
Job time : 21.6667 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:27:36 ; Search time 10.125 Seconds
 (without alignments)
 37.610 Million cell updates/sec

Title: US-09-228-866-5
 Perfect score: 9
 Sequence: 1 CNSRLQLRC 9

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 118358

Minimum DB seq length: 7
 Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	9	100.0	9	1	US-08-526-710-5	Sequence 5, Appli
2	9	100.0	9	3	US-08-862-855-5	Sequence 5, Appli
3	9	100.0	9	3	US-09-226-985-5	Sequence 5, Appli
4	9	100.0	9	4	US-09-227-906-5	Sequence 5, Appli
5	5	55.6	9	1	US-08-526-710-1	Sequence 1, Appli
6	5	55.6	9	3	US-08-862-855-1	Sequence 1, Appli
7	5	55.6	9	3	US-09-226-985-1	Sequence 1, Appli
8	5	55.6	9	4	US-09-227-906-1	Sequence 1, Appli
9	4	44.4	7	3	US-08-836-561-44	Sequence 44, Appli
10	4	44.4	7	3	US-08-328-239A-6	Sequence 6, Appli
11	4	44.4	7	4	US-09-434-122-44	Sequence 44, Appli

12	4	44.4	8	2	US-08-598-873-42	Sequence 42, Appl
13	4	44.4	8	3	US-09-258-754-256	Sequence 256, App
14	4	44.4	8	3	US-09-056-226-12	Sequence 12, Appl
15	4	44.4	8	3	US-09-042-107-256	Sequence 256, App
16	4	44.4	8	3	US-08-605-430-42	Sequence 42, Appl
17	4	44.4	10	1	US-08-466-434-1	Sequence 1, Appli
18	4	44.4	10	1	US-08-485-132-2	Sequence 2, Appli
19	4	44.4	10	3	US-08-888-158-2	Sequence 2, Appli
20	4	44.4	12	2	US-08-406-330-44	Sequence 44, Appl
21	4	44.4	12	2	US-08-556-597-44	Sequence 44, Appl
22	4	44.4	12	4	US-09-298-924-16	Sequence 16, Appl
23	4	44.4	12	4	US-09-690-454-89	Sequence 89, Appl
24	4	44.4	13	4	US-09-635-872A-34	Sequence 34, Appl
25	4	44.4	13	4	US-09-636-077A-34	Sequence 34, Appl
26	4	44.4	17	3	US-09-015-605-3	Sequence 3, Appli
27	4	44.4	17	4	US-09-523-899A-4	Sequence 4, Appli
28	4	44.4	18	1	US-07-995-503A-9	Sequence 9, Appli
29	4	44.4	18	1	US-08-390-510-9	Sequence 9, Appli
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31	4	44.4	18	2	US-08-390-509-9	Sequence 9, Appli
32	4	44.4	18	3	US-09-149-860A-9	Sequence 9, Appli
33	4	44.4	20	2	US-08-347-563A-21	Sequence 21, Appl
34	4	44.4	20	3	US-08-292-345B-21	Sequence 21, Appl
35	4	44.4	20	3	US-08-485-942A-21	Sequence 21, Appl
36	4	44.4	20	3	US-08-488-214A-21	Sequence 21, Appl
37	4	44.4	20	3	US-08-488-208A-21	Sequence 21, Appl
38	4	44.4	20	4	US-08-483-211A-21	Sequence 21, Appl
39	4	44.4	20	4	US-08-488-223A-21	Sequence 21, Appl
40	4	44.4	20	4	US-08-438-431A-21	Sequence 21, Appl
41	4	44.4	20	4	US-08-488-225A-21	Sequence 21, Appl
42	3	33.3	7	1	US-07-872-644-9	Sequence 9, Appli
43	3	33.3	7	1	US-08-297-494-9	Sequence 9, Appli
44	3	33.3	7	1	US-08-297-510-9	Sequence 9, Appli
45	3	33.3	7	1	US-08-526-710-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-08-526-710-5
; Sequence 5, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-5

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Query Match          100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CNSRLQLRC 9
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Db      1 CNSRLQLRC 9

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RESULT 2

US-08-862-855-5

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; Sequence 5, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-5

```

```

Query Match          100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CNSRLQLRC 9
        |||||
Db      1 CNSRLQLRC 9

```

```

RESULT 3
US-09-226-985-5
; Sequence 5, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```



```

; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-5

```

```

Query Match          100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 CNSRLQLRC 9
        |||||
Db      1 CNSRLQLRC 9

```

RESULT 4

```

US-09-227-906-5
; Sequence 5, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-5

```

```

Query Match          100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 CNSRLQLRC 9
        |||||
Db      1 CNSRLQLRC 9

```

```

RESULT 5
US-08-526-710-1
; Sequence 1, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/526,710
 ; FILING DATE: 11-SEP-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 1779
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-526-710-1

Query Match 55.6%; Score 5; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRL 5
 |||||
 Db 1 CNSRL 5

RESULT 6

US-08-862-855-1

; Sequence 1, Application US/08862855
 ; Patent No. 6068829
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: Method of Identifying Molecules That
 ; TITLE OF INVENTION: Home to a Selected Organ In Vivo
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/862,855
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/526,710
 ; FILING DATE: 11-SEP-1995
 ; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-1

```

```

Query Match          55.6%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 CNSRL 5
        |||||
Db      1 CNSRL 5

```

RESULT 7

US-09-226-985-1

```

; Sequence 1, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-1

```

```

Query Match          55.6%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CNSRL 5
        |||||
Db      1 CNSRL 5

```

RESULT 8

US-09-227-906-1

```

; Sequence 1, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-1

```

```

Query Match          55.6%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CNSRL 5
        |||||
Db      1 CNSRL 5

```

RESULT 9

```

US-08-836-561-44
; Sequence 44, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-561-44

```

```

Query Match          44.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SRLQ 6
        ||||
Db      3 SRLQ 6

```

RESULT 10

US-08-328-239A-6

```

; Sequence 6, Application US/08328239A
; Patent No. 6037136
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Galationov, Konstantin
; APPLICANT: Jesus, Catherine
; TITLE OF INVENTION: Interactions between Raf Proto-Oncogenes
; TITLE OF INVENTION: and CDC25 Phosphatases, and Uses Related Thereto
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,239A

```

```

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSV002.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-328-239A-6

```

```

Query Match          44.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SRLQ 6
        ||||
Db      2 SRLQ 5

```

```

RESULT 11
US-09-434-122-44
; Sequence 44, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
;            FURUYA, Akiko
;            NAKAMURA, Kazuyasu
;            IIDA, Akihiro
;            ANAZAWA, Hideharu
;            HANAI, No. 6538111uo
;            TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
;                    Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-No. 6538111-1999

```



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-434-122-44

```

```

Query Match          44.4%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 SRLQ 6
        ||||
Db      3 SRLQ 6

```

```

RESULT 12
US-08-598-873-42
; Sequence 42, Application US/08598873
; Patent No. 5928884
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996

```

```

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebel, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-598-873-42

```

```

Query Match          44.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 RLQL 7
        ||||
Db      5 RLQL 8

```

```

RESULT 13
US-09-258-754-256
; Sequence 256, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-256

```

```

Query Match          44.4%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CNSR 4
        ||||

```

Db 1 CNSR 4

RESULT 14

US-09-056-226-12

; Sequence 12, Application US/09056226B
; Patent No. 6177614
; GENERAL INFORMATION:
; APPLICANT: Colasanti, Joseph J.
; APPLICANT: Sundaresan, Venkatesan
; TITLE OF INVENTION: Control of Floral Induction in Plants
; TITLE OF INVENTION: and Uses Therefor
; FILE REFERENCE: CSHL94-04A4
; CURRENT APPLICATION NUMBER: US/09/056,226B
; CURRENT FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: US 09/000,640
; EARLIER FILING DATE: 1997-12-30
; EARLIER APPLICATION NUMBER: US 08/804,104
; EARLIER FILING DATE: 1997-02-20
; EARLIER APPLICATION NUMBER: PCT/US96/03466
; EARLIER FILING DATE: 1996-03-15
; EARLIER APPLICATION NUMBER: US 08/406,186
; EARLIER FILING DATE: 1995-03-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Zea mays
US-09-056-226-12

Query Match 44.4%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
|||
Db 5 SRLQ 8

RESULT 15

US-09-042-107-256

; Sequence 256, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 8
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-256

Query Match 44.4%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSR 4
|||
Db 1 CNSR 4

Search completed: November 13, 2003, 10:41:55
Job time : 11.125 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 09:53:11 ; Search time 28.875 Seconds
(without alignments)
49.473 Million cell updates/sec

Title: US-09-228-866-5
Perfect score: 9
Sequence: 1 CNSRLQLRC 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 358712

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	9	100.0		9	18	AAW13411	Brain homing pepti
2	9	100.0		9	21	AAB07391	Brain homing pepti
3	9	100.0		9	22	AAE11797	Phage peptide #5 t
4	9	100.0		9	23	AAU10708	Brain homing pepti
5	5	55.6		9	18	AAW13410	Brain homing pepti
6	5	55.6		9	21	AAB07387	Brain homing pepti
7	5	55.6		9	22	AAE11793	Phage peptide #1 t
8	5	55.6		9	23	AAU10704	Brain homing pepti
9	5	55.6		9	24	ABU59529	Brain receptor tar
10	5	55.6		16	24	ABP83048	G protein-coupled
11	5	55.6		17	23	AAU11633	Neuregulin-2 immun
12	5	55.6		18	23	AAM52964	Human thrombopoiet
13	5	55.6		18	23	AAM52965	Thrombopoietin rec
14	5	55.6		21	23	AAM52958	Generic thrombopoi
15	4	44.4		7	18	AAW27419	CDR2 from light ch
16	4	44.4		7	20	AAY16941	Heat shock protein
17	4	44.4		7	20	AAY05017	Tumour antigen ant
18	4	44.4		7	22	AAU72083	Melanoma antigen,
19	4	44.4		7	22	AAU25782	Breast cancer-asso
20	4	44.4		7	22	AAG63621	Complementarity de
21	4	44.4		7	22	AAM43951	H11 binding site c
22	4	44.4		7	22	AAM43956	H11 binding site c
23	4	44.4		7	22	AAM44290	H11 binding site c
24	4	44.4		7	22	AAM44295	H11 binding site c
25	4	44.4		7	22	AAM44300	H11 binding site c
26	4	44.4		7	22	AAM44896	H11 binding site c
27	4	44.4		7	22	AAM45075	H11 binding site c
28	4	44.4		7	22	AAM45259	H11 binding site c
29	4	44.4		7	22	AAM45264	H11 binding site c
30	4	44.4		7	22	AAM45401	H11 binding site c
31	4	44.4		7	22	AAM45628	H11 binding site c
32	4	44.4		7	22	AAM45827	H11 binding site c
33	4	44.4		7	22	AAM45872	H11 binding site c
34	4	44.4		7	22	AAM45877	H11 binding site c
35	4	44.4		7	22	AAM46507	H11 binding site c
36	4	44.4		7	22	AAB84974	Clone 2 scFv CDR L
37	4	44.4		7	22	AAB84986	G12 scFv CDR L2 re
38	4	44.4		7	22	AAB49817	Human endostatin p
39	4	44.4		7	22	AAB49818	Human endostatin p
40	4	44.4		7	22	AAB49819	Human endostatin p
41	4	44.4		7	23	AAU80633	Javelin peptide #6
42	4	44.4		7	24	ABP56502	S. pneumoniae PPS-
43	4	44.4		8	20	AAY32116	Maize id gene null
44	4	44.4		8	20	AAY48874	Membrane dipeptida
45	4	44.4		8	21	AAY69084	Subsequence which

ALIGNMENTS

RESULT 1

AAW13411

ID AAW13411 standard; Peptide; 9 AA.

XX

AC AAW13411;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;
KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in
PT vivo panning method, specifically to identify brain, kidney,
PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 11; Page 67; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing
CC peptide that was identified using a novel method for obtaining
CC molecules that home to a selected organ or tissue. This in vivo
CC panning method typically involves administering a phage display
CC library to a subject, and identifying expressed peptides which
CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
CC vascular tissue or tumour tissue. The isolated peptides (see
CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
CC labels to the selected organ/tissue (claimed) or to identify and/or
CC isolate target molecules (claimed). The peptides can be directly
CC identified in vivo, as compared to prior art in vitro screening
CC methods, which require further examination to see if they maintain
CC specificity in vivo.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 18; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNSRLQLRC 9

Db |||||
 1 CNSRLQLRC 9

RESULT 2

AAB07391

ID AAB07391 standard; peptide; 9 AA.

XX

AC AAB07391;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 5.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..9

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in

PT vivo panning comprises administering a library of diverse peptides

PT linked to a tag which facilitates recovery of these peptides -

XX

PS Example 2; Column 17; 20pp; English.

XX

CC The present sequence is a mouse brain homing peptide. This sequence was

CC identified by using in vivo panning to screen a library of potential

CC organ homing molecules. The present sequence can be used to direct a

CC moiety to a the brain tissue, by linking the moiety to the present

CC sequence. Examples of potential moieties are drugs, toxins or a

CC detectable label. The present sequence contains a SRL amino acid motif.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRLQLRC 9

Db

|||||||
1 CNSRLQLRC 9

RESULT 3

AAE11797

ID AAE11797 standard; peptide; 9 AA.

XX

AC AAE11797;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #5 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;

KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

FH Key Location/Qualifiers

FT Domain 3..5

FT /label= SRL_motif

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo

PT panning that selectively home to a selected organ or tissue useful for

PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRLQLRC 9
|||
Db 1 CNSRLQLRC 9

RESULT 4

AAU10708

ID AAU10708 standard; peptide; 9 AA.

XX

AC AAU10708;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #5 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;

KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.

XX

PT Recovering molecules that home to an organ or tissue, useful for

PT identifying molecules that home to a specific organ or tissue, e.g.

PT identifying a tumour homing molecule to identify the presence of cancer,

PT by in vivo panning of a library -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering
CC to the subject the library of diverse molecules, collecting a sample of
CC the selected organ or tissue (e.g. brain or kidney), and recovering from
CC the sample several molecules that home to the selected organ or tissue.
CC The method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety

CC (e.g. drug, toxin or detectable label) to the selected organ.
CC Specifically, the method is useful for identifying the presence of cancer
CC in a subject by linking an appropriate moiety to a tumour homing
CC molecule. The present method provides a direct means for identifying
CC molecules that specifically home to a selected organ and, therefore
CC provides a significant advantage over previous methods, which require
CC that a molecule identified using an in vitro screening method
CC subsequently be examined to determine if it maintains its specificity in
CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
CC the present invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRLQLRC 9
|||
Db 1 CNSRLQLRC 9

RESULT 5

AAW13410

ID AAW13410 standard; Peptide; 9 AA.

XX

AC AAW13410;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in
PT vivo panning method, specifically to identify brain, kidney,
PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 11; Page 67; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing
 CC peptide that was identified using a novel method for obtaining
 CC molecules that home to a selected organ or tissue. This in vivo
 CC panning method typically involves administering a phage display
 CC library to a subject, and identifying expressed peptides which
 CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
 CC vascular tissue or tumour tissue. The isolated peptides (see
 CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
 CC labels to the selected organ/tissue (claimed) or to identify and/or
 CC isolate target molecules (claimed). The peptides can be directly
 CC identified in vivo, as compared to prior art in vitro screening
 CC methods, which require further examination to see if they maintain
 CC specificity in vivo.

XX

SQ Sequence 9 AA;

Query Match 55.6%; Score 5; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRL 5
 |||||
 Db 1 CNSRL 5

RESULT 6

AAB07387

ID AAB07387 standard; peptide; 9 AA.

XX

AC AAB07387;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 1.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..9

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX
PT Identifying and recovering organ homing molecules or peptides by in
PT vivo panning comprises administering a library of diverse peptides
PT linked to a tag which facilitates recovery of these peptides -
XX
PS Example 2; Column 17; 20pp; English.
XX
CC The present sequence is a mouse brain homing peptide. This sequence was
CC identified by using in vivo panning to screen a library of potential
CC organ homing molecules. The present sequence can be used to direct a
CC moiety to a the brain tissue, by linking the moiety to the present
CC sequence. Examples of potential moieties are drugs, toxins or a
CC detectable label. The present sequence contains a SRL amino acid motif.
XX
SQ Sequence 9 AA;

Query Match 55.6%; Score 5; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRL 5
|||||
Db 1 CNSRL 5

RESULT 7
AAE11793

ID AAE11793 standard; peptide; 9 AA.
XX
AC AAE11793;
XX
DT 18-DEC-2001 (first entry)
XX
DE Phage peptide #1 targetted to brain.
XX
KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
XX
OS Bacteriophage.
XX
FH Key Location/Qualifiers
FT Domain 3..5
FT /label= SRL_motif
XX
PN US6296832-B1.
XX
PD 02-OCT-2001.
XX
PF 08-JAN-1999; 99US-0226985.
XX
PR 23-JUN-1997; 97US-0862855.
PR 11-SEP-1995; 95US-0526710.
PR 10-MAR-1997; 97US-0813273.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti E, Pasqualini R;

XX
 DR WPI; 2001-610691/70.
 XX
 PT Enriched library fraction comprising molecules recovered by in vivo
 PT panning that selectively home to a selected organ or tissue useful for
 PT treating disease or in diagnostic methods -
 XX
 PS Example 2; Column 17; 21pp; English.
 XX
 CC The invention relates to an enriched library fraction containing
 CC molecules that selectively home to a selected organ or tissue such as
 CC brain, kidney or tumour recovered by in vivo panning. The invention
 CC generally relates to the field of molecular medicine, drug delivery and
 CC to a method of invivo panning for identifying a molecule that homes to a
 CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
 CC and fragments of proteins contained in an enriched library fraction may
 CC be administered to a subject as part of a pharmaceutical composition to
 CC treat disease or in diagnostic methods. The present sequence is a
 CC peptide from bacteriophage targetted to brain.
 XX
 SQ Sequence 9 AA;

Query Match 55.6%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRL 5
 |||||
 Db 1 CNSRL 5

RESULT 8
 AAU10704
 ID AAU10704 standard; peptide; 9 AA.
 XX
 AC AAU10704;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Brain homing peptide #1 useful for delivery of target molecules.
 XX
 KW Organ targeting; tissue targeting; cancer; tumour homing molecule;
 KW delivery of target molecule; brain homing peptide.
 XX
 OS Synthetic.
 XX
 PN US6306365-B1.
 XX
 PD 23-OCT-2001.
 XX
 PF 08-JAN-1999; 99US-0227906.
 XX
 PR 23-JUN-1997; 97US-0862855.
 PR 11-SEP-1995; 95US-0526710.
 PR 10-MAR-1997; 97US-0813273.
 XX
 PA (BURN-) BURNHAM INST.

XX
 PI Ruoslahti E, Pasqualini R;
 XX
 DR WPI; 2002-040196/05.
 XX
 PT Recovering molecules that home to an organ or tissue, useful for
 PT identifying molecules that home to a specific organ or tissue, e.g.
 PT identifying a tumour homing molecule to identify the presence of cancer,
 PT by in vivo panning of a library -
 XX
 PS Example 2; Column 17; 21pp; English.
 XX
 CC The present invention relates to a method of recovering molecules that
 CC home to a selected organ or tissue. The method comprises administering
 CC to the subject the library of diverse molecules, collecting a sample of
 CC the selected organ or tissue (e.g. brain or kidney), and recovering from
 CC the sample several molecules that home to the selected organ or tissue.
 CC The method is useful for identifying molecules, particularly useful for
 CC screening large number of molecules (e.g. peptides), that home to a
 CC specific organ. The identified molecule is useful for e.g. raising an
 CC antibody specific for a target molecule, targeting a desired moiety
 CC (e.g. drug, toxin or detectable label) to the selected organ.
 CC Specifically, the method is useful for identifying the presence of cancer
 CC in a subject by linking an appropriate moiety to a tumour homing
 CC molecule. The present method provides a direct means for identifying
 CC molecules that specifically home to a selected organ and, therefore
 CC provides a significant advantage over previous methods, which require
 CC that a molecule identified using an in vitro screening method
 CC subsequently be examined to determine if it maintains its specificity in
 CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
 CC the present invention.
 XX
 SQ Sequence 9 AA;

Query Match 55.6%; Score 5; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNSRL 5
 |||||
 Db 1 CNSRL 5

RESULT 9
 ABU59529
 ID ABU59529 standard; Peptide; 9 AA.
 XX
 AC ABU59529;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Brain receptor targeting peptide #1.
 XX
 KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
 KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
 KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
 KW tumour; cationic cancer-targeting peptide.

XX
 OS Synthetic.
 XX
 PN US2002041898-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 25-JUL-2001; 2001US-0912609.
 XX
 PR 05-JAN-2000; 2000US-0478124.
 PR 31-OCT-2000; 2000US-0703474.
 XX
 PA (UNGE/) UNGER E C.
 PA (MATS/) MATSUNAGA T O.
 PA (RAMA/) RAMASWAMI V.
 PA (ROMA/) ROMANOWSKI M J.
 XX
 PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 XX
 DR WPI; 2003-208921/20.
 XX
 PT Targeted delivery system comprising a bioactive agent homogeneously
 PT dispersed in a targeted matrix is especially useful in cancer therapy
 PT -
 XX
 PS Claim 23; Page 37; 46pp; English.
 XX
 CC The invention relates to a composition comprising a bioactive agent
 CC homogeneously dispersed in a targeted matrix (polymer and targeting
 CC ligand). Also included are a targeted matrix for use as a delivery
 CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration
 CC of the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.
 CC Examples of targeting peptides are disclosed including cathepsin-D
 CC substrate peptides, peptides targeting receptors in the brain and
 CC kidney, peptides recognising fibronectin- and vitronectin-binding
 CC integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g.,
 CC antibodies, peptides targeting the angiogenic endothelium of solid
 CC tumours, tissue specific peptides (e.g. of lung, skin, pancreas,
 CC intestine, uterus, adrenal gland and retina), and cationic cancer-
 CC targeting peptides. The present sequence is a peptide targeting
 CC ligand disclosed in the invention.
 XX
 SQ Sequence 9 AA;

 Query Match 55.6%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CNSRL 5
 |||||
 Db 1 CNSRL 5

RESULT 10

ABP83048
ID ABP83048 standard; Peptide; 16 AA.
XX
AC ABP83048;
XX
DT 04-MAR-2003 (first entry)
XX
DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1721.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Claim 1; Fig 2; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative

CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

XX

SQ Sequence 16 AA;

Query Match 55.6%; Score 5; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQL 7

|||||

Db 1 SRLQL 5

RESULT 11

AAU11633

ID AAU11633 standard; Peptide; 17 AA.

XX

AC AAU11633;

XX

DT 12-MAR-2002 (first entry)

XX

DE Neuregulin-2 immunogenic peptide K71984M.

XX

KW Human; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;

KW cell survival; cell growth; cell differentiation; erbB receptor;

KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;

KW atherosclerosis; vascular lesion; vascular hypertension;

KW degenerative congenital vascular disease; myasthenia gravis;

KW neurodegenerative disorder; peripheral neuropathy; rat;

KW sensory nerve fiber neuropathy; motor fiber neuropathy;

KW sensory nerve fiber neuropathy; multiple sclerosis; K71984M;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;

KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;

KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.

XX

OS Homo sapiens.

OS Rattus sp.

XX

PN WO200189568-A1.

XX

PD 29-NOV-2001.

XX

PF 23-MAY-2001; 2001WO-US16896.

XX

PR 23-MAY-2000; 2000US-206495P.

XX

PA (CENE-) CENES PHARM INC.

XX

PI Marchionni MA;

XX

DR WPI; 2002-097612/13.

XX

PT Neuregulin-2 polypeptide and polynucleotide useful for treating
PT multiple sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
PT disease, by increasing mitogenesis, survival, growth or differentiation
PT of a cell -

XX

PS Example 5; Page 36; 79pp; English.

XX

CC The invention relates to a substantially pure neuregulin (NRG)-2
CC polypeptide comprising or consisting of a sequence for human
CC NRG-2alpha or NRG-2beta (clone 2b7) and the polynucleotides encoding
CC the. Also included are a vector expressing the protein, a host cell
CC comprising the vector, a transgenic non-human animal transformed with
CC the vector or having a knockout mutation in one or both NRG-2
CC alleles and an anti-NRG-2 antibody. Analysis of mutations in NRG-2 in an
CC individual is useful for diagnosing an increased likelihood of
CC developing a NRG-2-related disease or condition in a test subject.
CC NRG-2 is useful for increasing the mitogenesis, survival, growth or
CC differentiation of a cell (e.g. a neuronal cell), where the cell
CC expresses an erbB receptor. NRG-2 is useful for treating diseases
CC and disorders such as cardiomyopathy (preferably degenerative congenital
CC disease), ischaemic damage, cardiac trauma or heart failure or which
CC has a condition affecting smooth muscle which include atherosclerosis,
CC vascular lesion, vascular hypertension, and degenerative congenital
CC vascular disease, myasthenia gravis, a neurodegenerative disorder,
CC peripheral neuropathy, a sensory nerve fiber neuropathy, a motor fiber
CC and a sensory nerve fiber neuropathy, multiple sclerosis, amyotrophic
CC lateral sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
CC disease, Parkinson's disease, cerebellar ataxia, and spinal cord injury.
CC The antibody is useful for treatment of a tumour comprising inhibiting
CC proliferation of a tumour cell preferably a glial tumour cell, for
CC treating of neurofibromatosis by inhibiting glial cell mitogenesis.
CC The present sequence represents an immunogenic peptide designed
CC from rat and human NRG-2.

XX

SQ Sequence 17 AA;

Query Match 55.6%; Score 5; DB 23; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSRLQ 6

|||||

Db 1 NSRLQ 5

RESULT 12

AAM52964

ID AAM52964 standard; peptide; 18 AA.

XX

AC AAM52964;

XX

DT 12-MAR-2002 (first entry)
XX
DE Human thrombopoietin receptor peptide (TPO-Rp) G4-R21, SEQ ID NO:5.
XX
KW Thrombopoietin receptor peptide; TPO-Rp; TPO-R agonist; activation;
KW TPO utilisation; platelet count; thrombocytopenia; idiopathic;
KW bone marrow transplantation; radiotherapy; chemotherapy;
KW allergic reaction; haematological disorder; human.
XX
OS Homo sapiens.
XX
PN EP1149906-A1.
XX
PD 31-OCT-2001.
XX
PF 25-APR-2000; 2000EP-0108075.
XX
PR 25-APR-2000; 2000EP-0108075.
XX
PA (PLIV) PLIVA FARMACEUTSKA IND DIONICKO DRUST.
XX
PI Naranda T, Olssen L;
XX
DR WPI; 2002-063467/09.
XX
PT Novel oligopeptides with thrombopoietin receptor modulatory activity,
PT useful for the treatment or diagnosis of hematological disorders,
PT especially thrombocytopenia -
XX
PS Claim 2; Page -; 39pp; English.
XX
CC The invention relates to novel oligopeptides derived from the
CC thrombopoietin receptor (TPO-R). The thrombopoietin receptor-derived
CC peptides (TPO-Rp) are derived from residues 444-464 of the human
CC TPO-R, and are able to modulate TPO-R activity. The TPO-R peptides
CC (TPO-Rp) have the generic formula:
CC X1-Gly-Thr-Leu-Glu-Leu-X2-Ser-X2-Tyr-Arg-Thr-Leu-Gln-Leu-X3, where:
CC X1 is the sequence Ala-Arg-Gly or is absent;
CC X2 is Arg or Ala; and
CC X3 is the sequence Arg-Ala-Arg or is absent.
CC The peptides of the invention strongly bind to and activate TPO-R, and
CC also improve the utilisation of endogenous TPO, and can thus be used to
CC increase platelet count. The TPO-Rp peptides may be used in the treatment
CC of thrombocytopenia, particularly thrombocytopenia resulting from bone
CC marrow transplantation, radiotherapy, chemotherapy, allergic reactions
CC or which are are idiopathic, and other haematological disorders.
CC The peptides are non-toxic and stable, provide a safe treatment of
CC thrombocytopenia and show high potency (e.g., activity at nanomolar to
CC micromolar concentrations). They do not reduce sensitivity to TPO, but
CC may have a synergistic effect in combination with TPO. The present
CC sequence represents a peptide of the invention, designated TPO-Rp G4-R21.
CC Note: The present sequence is not shown in full in the specification,
CC but was derived from the full-length human TPO-Rp sequence shown on
CC page 14 (AAM52959).
XX
SQ Sequence 18 AA;

Query Match 55.6%; Score 5; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RLQLR 8
|||
Db 12 RLQLR 16

RESULT 13

AAM52965

ID AAM52965 standard; peptide; 18 AA.

XX

AC AAM52965;

XX

DT 12-MAR-2002 (first entry)

XX

DE Thrombopoietin receptor peptide (TPO-Rp) G4-R21 (R9A, R11A), SEQ ID NO:6.

XX

KW Thrombopoietin receptor peptide; TPO-Rp; TPO-R agonist; activation;

KW TPO utilisation; platelet count; thrombocytopenia; idiopathic;

KW bone marrow transplantation; radiotherapy; chemotherapy;

KW allergic reaction; haematological disorder; human; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 6

FT /note= "Ala replaces wild-type Arg"

FT Misc-difference 8

FT /note= "Ala replaces wild-type Arg"

XX

PN EP1149906-A1.

XX

PD 31-OCT-2001.

XX

PF 25-APR-2000; 2000EP-0108075.

XX

PR 25-APR-2000; 2000EP-0108075.

XX

PA (PLIV) PLIVA FARMACEUTSKA IND DIONICKO DRUST.

XX

PI Naranda T, Olssen L;

XX

DR WPI; 2002-063467/09.

XX

PT Novel oligopeptides with thrombopoietin receptor modulatory activity,

PT useful for the treatment or diagnosis of hematological disorders,

PT especially thrombocytopenia -

XX

PS Claim 2; Page -; 39pp; English.

XX

CC The invention relates to novel oligopeptides derived from the

CC thrombopoietin receptor (TPO-R). The thrombopoietin receptor-derived

CC peptides (TPO-Rp) are derived from residues 444-464 of the human

CC TPO-R, and are able to modulate TPO-R activity. The TPO-R peptides

CC (TPO-Rp) have the generic formula:
 CC X1-Gly-Thr-Leu-Glu-Leu-X2-Ser-X2-Tyr-Arg-Thr-Leu-Gln-Leu-X3, where:
 CC X1 is the sequence Ala-Arg-Gly or is absent;
 CC X2 is Arg or Ala; and
 CC X3 is the sequence Arg-Ala-Arg or is absent.
 CC The peptides of the invention strongly bind to and activate TPO-R, and
 CC also improve the utilisation of endogenous TPO, and can thus be used to
 CC increase platelet count. The TPO-Rp peptides may be used in the treatment
 CC of thrombocytopenia, particularly thrombocytopenia resulting from bone
 CC marrow transplantation, radiotherapy, chemotherapy, allergic reactions
 CC or which are are idiopathic, and other haematological disorders.
 CC The peptides are non-toxic and stable, provide a safe treatment of
 CC thrombocytopenia and show high potency (e.g., activity at nanomolar to
 CC micromolar concentrations). They do not reduce sensitivity to TPO, but
 CC may have a synergistic effect in combination with TPO. The present
 CC sequence represents a peptide of the invention, designated TPO-Rp G4-R21.
 CC (R9A, R11A).
 CC Note: The present sequence is not shown in full in the specification,
 CC but was derived from the full-length human TPO-Rp sequence shown on
 CC page 14 (AAM52959).
 XX
 SQ Sequence 18 AA;

Query Match 55.6%; Score 5; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQLR 8
 |||||
 Db 12 RLQLR 16

RESULT 14

AAM52958

ID AAM52958 standard; peptide; 21 AA.

XX

AC AAM52958;

XX

DT 12-MAR-2002 (first entry)

XX

DE Generic thrombopoietin receptor peptide (TPO-Rp).

XX

KW Thrombopoietin receptor peptide; TPO-Rp; TPO-R agonist; activation;

KW TPO utilisation; platelet count; thrombocytopenia; idiopathic;

KW bone marrow transplantation; radiotherapy; chemotherapy;

KW allergic reaction; haematological disorder; human; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1..3

FT /note= "These 3 residues are optionally absent"

FT Misc-difference 9

FT /label= Ala, Arg

FT Misc-difference 11

FT /label= Ala, Arg

FT Misc-difference 19..21
 FT /note= "These 3 residues are optionally absent"
 XX
 PN EP1149906-A1.
 XX
 PD 31-OCT-2001.
 XX
 PF 25-APR-2000; 2000EP-0108075.
 XX
 PR 25-APR-2000; 2000EP-0108075.
 XX
 PA (PLIV) PLIVA FARMACEUTSKA IND DIONICKO DRUST.
 XX
 PI Naranda T, Olssen L;
 XX
 DR WPI; 2002-063467/09.
 XX
 PT Novel oligopeptides with thrombopoietin receptor modulatory activity,
 PT useful for the treatment or diagnosis of hematological disorders,
 PT especially thrombocytopenia -
 XX
 PS Claim 1; Page -; 39pp; English.
 XX
 CC The invention relates to novel oligopeptides derived from the
 CC thrombopoietin receptor (TPO-R). The thrombopoietin receptor-derived
 CC peptides (TPO-Rp) are derived from residues 444-464 of the human
 CC TPO-R, and are able to modulate TPO-R activity. The TPO-R peptides
 CC (TPO-Rp) have the generic formula:
 CC X1-Gly-Thr-Leu-Glu-Leu-X2-Ser-X2-Tyr-Arg-Thr-Leu-Gln-Leu-X3, where:
 CC X1 is the sequence Ala-Arg-Gly or is absent;
 CC X2 is Arg or Ala; and
 CC X3 is the sequence Arg-Ala-Arg or is absent.
 CC The peptides of the invention strongly bind to and activate TPO-R, and
 CC also improve the utilisation of endogenous TPO, and can thus be used to
 CC increase platelet count. The TPO-Rp peptides may be used in the treatment
 CC of thrombocytopenia, particularly thrombocytopenia resulting from bone
 CC marrow transplantation, radiotherapy, chemotherapy, allergic reactions
 CC or which are idiopathic, and other haematological disorders.
 CC The peptides are non-toxic and stable, provide a safe treatment of
 CC thrombocytopenia and show high potency (e.g., activity at nanomolar to
 CC micromolar concentrations). They do not reduce sensitivity to TPO, but
 CC may have a synergistic effect in combination with TPO. The present
 CC sequence represents a generic version of the peptides of the invention.
 CC Note: The present sequence is not shown in full in the specification,
 CC but was derived from the sequence shown on page 24 (Claim 1).
 XX
 SQ Sequence 21 AA;

Query Match 55.6%; Score 5; DB 23; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQLR 8
 |||||
 Db 15 RLQLR 19

RESULT 15

AAW27419

ID AAW27419 standard; peptide; 7 AA.

XX

AC AAW27419;

XX

DT 19-DEC-1997 (first entry)

XX

DE CDR2 from light chain variable region of KM1259 antibody.

XX

KW Complementarity determining region; CDR; light chain; treatment;

KW variable region; murine; mouse; human; interleukin 5; IL-5;

KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;

KW assay; diagnosis; allergic respiratory disease; chronic bronchitis;

XX

OS Mus spp.

XX

PN WO9710354-A1.

XX

PD 20-MAR-1997.

XX

PF 11-SEP-1996; 96WO-JP02588.

XX

PR 11-SEP-1995; 95JP-0232384.

XX

PA (KYOW) KYOWA HAKKO KOGYO KK.

XX

PI Anazawa H, Furuya A, Hanai N, Iida A, Koike M;

PI Nakamura K, Takatsu K;

XX

DR WPI; 1997-202249/18.

XX

PT Antibody against alpha-chain of human interleukin 5 receptor -

PT useful for diagnosis and treatment of respiratory allergic diseases,

PT e.g. chronic bronchitis

XX

PS Claim 8; Page 165; 238pp; Japanese.

XX

CC The present sequence is complementarity determining region 2 (CDR2)

CC from the light chain variable region of the murine anti-human

CC interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal

CC antibody (MAb) KM1259. KM1259 is produced by the hybridoma

CC FERM BP-5134, which was prepared by immunising Balb/c mice with

CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse

CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAb

CC can be used to detect or assay for hIL-5R alpha and cells

CC expressing it on their surface, especially to diagnose allergic

CC respiratory diseases, e.g. chronic bronchitis. It can also be used

CC to treat such diseases.

XX

SQ Sequence 7 AA;

Query Match 44.4%; Score 4; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6

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Job time : 29.875 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:38:27 ; Search time 17.625 Seconds
(without alignments)
93.222 Million cell updates/sec

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Title:      US-09-228-866-5
Perfect score: 9
Sequence:  1 CNSRLQLRRC 9
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 124183

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Minimum DB seq length: 7
Maximum DB seq length: 21
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Post-processing: Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	55.6	9	12	US-10-306-878-11	Sequence 11, Appl
2	5	55.6	16	15	US-10-225-567A-1721	Sequence 1721, Ap
3	5	55.6	17	9	US-09-864-675-17	Sequence 17, Appl
4	5	55.6	18	12	US-10-258-565-5	Sequence 5, Appli
5	5	55.6	18	12	US-10-258-565-6	Sequence 6, Appli
6	5	55.6	18	12	US-10-029-386-32770	Sequence 32770, A
7	4	44.4	7	9	US-09-192-854-16	Sequence 16, Appl
8	4	44.4	7	9	US-09-192-854-43	Sequence 43, Appl
9	4	44.4	7	9	US-09-192-854-88	Sequence 88, Appl
10	4	44.4	7	9	US-09-192-854-101	Sequence 101, App
11	4	44.4	7	9	US-09-192-854-126	Sequence 126, App
12	4	44.4	7	9	US-09-192-854-130	Sequence 130, App
13	4	44.4	7	9	US-09-192-854-145	Sequence 145, App
14	4	44.4	7	10	US-09-968-561A-23	Sequence 23, Appl
15	4	44.4	7	10	US-09-968-561A-65	Sequence 65, Appl
16	4	44.4	7	10	US-09-968-561A-113	Sequence 113, App
17	4	44.4	7	10	US-09-968-561A-155	Sequence 155, App
18	4	44.4	7	10	US-09-968-561A-161	Sequence 161, App
19	4	44.4	7	10	US-09-968-561A-167	Sequence 167, App
20	4	44.4	7	10	US-09-968-561A-173	Sequence 173, App
21	4	44.4	7	10	US-09-968-561A-179	Sequence 179, App
22	4	44.4	7	10	US-09-968-561A-203	Sequence 203, App
23	4	44.4	7	10	US-09-968-561A-227	Sequence 227, App
24	4	44.4	7	10	US-09-968-561A-233	Sequence 233, App
25	4	44.4	7	10	US-09-968-561A-257	Sequence 257, App
26	4	44.4	7	11	US-09-977-797A-34	Sequence 34, Appl
27	4	44.4	7	12	US-10-052-578-211	Sequence 211, App
28	4	44.4	7	12	US-09-968-744A-23	Sequence 23, Appl
29	4	44.4	7	12	US-09-968-744A-65	Sequence 65, Appl
30	4	44.4	7	12	US-09-968-744A-113	Sequence 113, App
31	4	44.4	7	12	US-09-968-744A-155	Sequence 155, App
32	4	44.4	7	12	US-09-968-744A-161	Sequence 161, App
33	4	44.4	7	12	US-09-968-744A-167	Sequence 167, App
34	4	44.4	7	12	US-09-968-744A-173	Sequence 173, App
35	4	44.4	7	12	US-09-968-744A-179	Sequence 179, App
36	4	44.4	7	12	US-09-968-744A-203	Sequence 203, App
37	4	44.4	7	12	US-09-968-744A-227	Sequence 227, App
38	4	44.4	7	12	US-09-968-744A-233	Sequence 233, App
39	4	44.4	7	12	US-09-968-744A-257	Sequence 257, App
40	4	44.4	7	12	US-10-203-754A-11	Sequence 11, Appl
41	4	44.4	7	12	US-10-053-520-211	Sequence 211, App
42	4	44.4	7	12	US-10-053-498B-211	Sequence 211, App
43	4	44.4	7	15	US-10-283-349-44	Sequence 44, Appl
44	4	44.4	7	15	US-10-227-616-54	Sequence 54, Appl
45	4	44.4	8	12	US-10-022-066-202	Sequence 202, App

ALIGNMENTS

RESULT 1

US-10-306-878-11

```
; Sequence 11, Application US/10306878
; Publication No. US20030175819A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
; TITLE OF INVENTION: Methods for Identifying Modulators of
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: P-LJ 5535
; CURRENT APPLICATION NUMBER: US/10/306,878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
```

US-10-306-878-11

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Query Match          55.6%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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Qy      1 CNSRL 5
        |||||
Db      1 CNSRL 5
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RESULT 2

US-10-225-567A-1721

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; Sequence 1721, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1721
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-225-567A-1721

Query Match 55.6%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQL 7
|||||
Db 1 SRLQL 5

RESULT 3

US-09-864-675-17

; Sequence 17, Application US/09864675
; Patent No. US20020081286A1
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark
; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
; FILE REFERENCE: 04585/049002
; CURRENT APPLICATION NUMBER: US/09/864,675
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,495
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Rattus norvegicus and Homo sapiens
US-09-864-675-17

Query Match 55.6%; Score 5; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSRLQ 6
|||||
Db 1 NSRLQ 5

RESULT 4

US-10-258-565-5

; Sequence 5, Application US/10258565
; Publication No. US20030181659A1
; GENERAL INFORMATION:
; APPLICANT: PLIVA, farmaceutska industrija, dionicko drustvo
; TITLE OF INVENTION: Thrombopoietin Receptor Peptide
; FILE REFERENCE: 14267
; CURRENT APPLICATION NUMBER: US/10/258,565
; CURRENT FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-258-565-5

Query Match 55.6%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQLR 8
|||||
Db 12 RLQLR 16

RESULT 5

US-10-258-565-6

; Sequence 6, Application US/10258565
; Publication No. US20030181659A1
; GENERAL INFORMATION:
; APPLICANT: PLIVA, farmaceutska industrija, dionicko drustvo
; TITLE OF INVENTION: Thrombopoietin Receptor Peptide
; FILE REFERENCE: 14267
; CURRENT APPLICATION NUMBER: US/10/258,565
; CURRENT FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-565-6

Query Match 55.6%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQLR 8
|||||
Db 12 RLQLR 16

RESULT 6

US-10-029-386-32770

; Sequence 32770, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32770
; LENGTH: 18
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010168.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.6
US-10-029-386-32770

Query Match 55.6%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQL 7
 ||||
Db 4 SRLQL 8

RESULT 7

US-09-192-854-16
; Sequence 16, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-16

Query Match 44.4%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
 ||||
Db 3 SRLQ 6

RESULT 8

US-09-192-854-43
; Sequence 43, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17

; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-43

Query Match 44.4%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
|||
Db 3 SRLQ 6

RESULT 9

US-09-192-854-88
; Sequence 88, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-88

Query Match 44.4%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
|||
Db 3 SRLQ 6

RESULT 10

US-09-192-854-101
; Sequence 101, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides

; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-101

Query Match 44.4%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
|||
Db 3 SRLQ 6

RESULT 11

US-09-192-854-126
; Sequence 126, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-126

Query Match 44.4%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
|||
Db 3 SRLQ 6

RESULT 12

US-09-192-854-130
; Sequence 130, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:


```

; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-192-854-130

```

```

Query Match          44.4%;  Score 4;  DB 9;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 SRLQ 6
        ||||
Db      3 SRLQ 6

```

RESULT 13

```

US-09-192-854-145
; Sequence 145, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-192-854-145

```

```

Query Match          44.4%;  Score 4;  DB 9;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 SRLQ 6
        ||||
Db      3 SRLQ 6

```

RESULT 14

```

US-09-968-561A-23

```

```

; Sequence 23, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-23

```

```

Query Match          44.4%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 SRLQ 6
        ||||
Db      3 SRLQ 6

```

RESULT 15

US-09-968-561A-65

```

; Sequence 65, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20

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; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-65

Query Match 44.4%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
 ||||
Db 3 SRLQ 6

Search completed: November 13, 2003, 11:12:32
Job time : 17.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:26:01 ; Search time 8.8125 Seconds
(without alignments)
98.215 Million cell updates/sec

Title: US-09-228-866-5
Perfect score: 9
Sequence: 1 CNSRLQLRC 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3752

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	4	44.4	20	2	I54283	arylsulfatase A -	
2	3	33.3	8	2	S59622	metallothionein is	
3	3	33.3	8	2	T10077	hypothetical prote	
4	3	33.3	9	2	S13889	phosphoenolpyruvat	
5	3	33.3	10	2	PS0451	24K protein 4302	
6	3	33.3	10	2	PT0309	Ig heavy chain CRD	
7	3	33.3	11	2	PT0217	T-cell receptor be	
8	3	33.3	12	1	LFECPE	pyrE leader peptid	
9	3	33.3	12	2	A29169	phospholipase A2 (
10	3	33.3	12	2	E64573	hypothetical prote	
11	3	33.3	14	2	PS0371	hypothetical prote	
12	3	33.3	14	2	A35105	hypothetical prote	
13	3	33.3	14	2	I54284	C1-inhibitor - hum	
14	3	33.3	14	2	B61235	fibroblast-activat	
15	3	33.3	14	2	A43847	Ig mu chain V regi	
16	3	33.3	15	2	PQ0195	Sf11-glycoprotein	
17	3	33.3	15	2	I49420	placental lactogen	
18	3	33.3	15	2	S36891	ribosomal protein	
19	3	33.3	15	2	PA0029	protein QA100012 -	
20	3	33.3	15	2	PQ0192	stylar glycoprotei	
21	3	33.3	15	2	PQ0193	stylar glycoprotei	
22	3	33.3	15	2	G41299	T-cell receptor al	
23	3	33.3	15	2	F44823	synaptosomal-assoc	
24	3	33.3	15	2	PH0770	T-cell receptor be	
25	3	33.3	16	2	S35627	uvsX protein - pha	
26	3	33.3	16	2	S34444	blaZ protein - Sta	
27	3	33.3	16	2	A28587	T-cell receptor be	
28	3	33.3	17	2	JP0068	ribosomal protein	
29	3	33.3	17	2	E28587	T-cell receptor be	
30	3	33.3	17	2	A54205	heterogeneous ribo	
31	3	33.3	17	2	H53284	T-cell receptor be	
32	3	33.3	18	2	A36133	hypothetical prote	
33	3	33.3	18	2	A45138	arsenite oxidase I	
34	3	33.3	18	2	I50389	myosin heavy chain	
35	3	33.3	18	2	I46653	T-cell receptor de	
36	3	33.3	19	2	S63510	phosphonoacetaldeh	
37	3	33.3	19	2	PC1324	hypothetical prote	
38	3	33.3	19	2	PC1322	hypothetical prote	
39	3	33.3	19	2	PH1353	Ig heavy chain DJ	
40	3	33.3	20	2	PQ0751	self-incompatibili	
41	3	33.3	20	2	PH0111	style glycoprotein	
42	3	33.3	20	2	C20554	hemocyanin subunit	
43	3	33.3	20	2	H49034	nuclear antigen EB	
44	3	33.3	20	2	I67551	monocyte chemotact	
45	3	33.3	20	2	A41439	acid ribonuclease	

ALIGNMENTS

RESULT 1

I54283

arylsulfatase A - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C;Accession: I54283

R;Regis, S.; Carrozzo, R.; Filocamo, M.; Serra, G.; Mastropaolo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995

A;Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infantile metachromatic leukodystrophy patient.

A;Reference number: I54283; MUID:95362256; PMID:7635478

A;Accession: I54283

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-20 <RES>

A;Cross-references: GB:S78735; NID:g1037139; PIDN:AAB35013.1; PID:g1037140

Query Match 44.4%; Score 4; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQL 7

||||

Db 13 RLQL 16

RESULT 2

S59622

metallothionein isoform a, cadmium-binding - Arianta arbustorum (terrestrial snail) (fragment)

C;Species: Arianta arbustorum

C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999

C;Accession: S59622

R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Biochem. J. 311, 951-957, 1995

A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothionein isoforms from the terrestrial gastropod Arianta arbustorum.

A;Reference number: S59621; MUID:96067616; PMID:7487956

A;Accession: S59622

A;Molecule type: protein

A;Residues: 1-8 <BER>

C;Superfamily: metallothionein

C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 33.3%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNS 3

|||

Db 1 CNS 3

RESULT 3

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C;Species: Methylophilus methylotrophus
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T10077
 R;Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.
 J. Bacteriol. 176, 4073-4080, 1994
 A;Title: Organization of the methylamine utilization (mau) genes in
 Methylophilus methylotrophus W3A1-NS.
 A;Reference number: Z16936; MUID:94292427; PMID:8021188
 A;Accession: T10077
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-8 <CHI>
 A;Cross-references: EMBL:L26407; NID:g561931; PIDN:AAB46955.1; PID:g561933
 A;Experimental source: strain W3A1
 C;Genetics:
 A;Gene: mauN

Query Match 33.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQ 6
 |||
 Db 3 RLQ 5

RESULT 4

S13889

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

C;Species: Zea mays (maize)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

C;Accession: S13889

R;Jiao, J.; Chollet, R.

Arch. Biochem. Biophys. 283, 300-305, 1990

A;Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate
 carboxylase by a C(4)-leaf protein-serine kinase.

A;Reference number: S13889; MUID:91112741; PMID:2148863

A;Accession: S13889

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <JIA>

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 33.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
 |||
 Db 7 QLR 9

RESULT 5

PS0451

24K protein 4302 - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C;Accession: PS0451
R;Tsugita, A.; Kamo, M.
submitted to JIPID, April 1993
A;Reference number: PS0209
A;Accession: PS0451
A;Molecule type: protein
A;Residues: 1-10 <TSU>
A;Experimental source: callus, strain Nihonbare
C;Comment: molecular weight 24K, pI 5.5.

Query Match 33.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
|||
Db 5 QLR 7

RESULT 6

PT0309

Ig heavy chain CRD3 region (clone 6-94) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0309

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0309

A;Molecule type: DNA

A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSR 4
|||
Db 5 NSR 7

RESULT 7

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not
restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
|||
Db 3 SRL 5

RESULT 8

LFECPE

pyrE leader peptide - Escherichia coli

C;Species: Escherichia coli

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Mar-1993

C;Accession: A30400; A05110; Q00495

R;Poulsen, P.; Bonekamp, F.; Jensen, K.F.

EMBO J. 3, 1783-1790, 1984

A;Title: Structure of the Escherichia coli pyrE operon and control of pyrE expression by a UTP modulated intercistronic attenuation.

A;Reference number: A30400; MUID:85003588; PMID:6207018

A;Accession: A30400

A;Molecule type: DNA

A;Residues: 1-12 <POU1>

R;Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.
Eur. J. Biochem. 135, 223-229, 1983

A;Title: Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front of the protein-coding region.

A;Reference number: A05110; MUID:83287414; PMID:6349999

A;Accession: A05110

A;Molecule type: DNA

A;Residues: 1-12 <POU2>

C;Genetics:

A;Gene: pyrE-LP

A;Map position: 82 min

C;Superfamily: pyrE leader peptide

Query Match 33.3%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
|||
Db 2 SRL 4

RESULT 9

A29169

phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997

C;Accession: A29169

R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Biochem. 53, 91-97, 1975

A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.

A;Reference number: A94661

A;Accession: A29169

A;Molecule type: protein

A;Residues: 1-12 <DUT>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSR 4

|||

Db 5 NSR 7

RESULT 10

E64573

hypothetical protein HP0429 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C;Accession: E64573

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald,
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;
Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;
Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: E64573

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-12 <TOM>

A;Cross-references: GB:AE000559; GB:AE000511; NID:g2313536; PIDN:AAD07512.1;
PID:g2313552; TIGR:HP0429

Query Match 33.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQL 7

|||

Db 10 LQL 12

RESULT 11

PS0371

hypothetical protein (psaC region) - Synechococcus sp. (fragment)

C;Species: *Synechococcus* sp.
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C;Accession: PS0371
 R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
 Gene 112, 123-128, 1992
 A;Title: The *psaC* genes of *Synechococcus* sp. PCC7002 and *Cyanophora paradoxa*: cloning and sequence analysis.
 A;Reference number: JS0694; MUID:92201692; PMID:1551590
 A;Accession: PS0371
 A;Molecule type: DNA
 A;Residues: 1-14 <RHI>
 A;Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match 33.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQ 6
 |||
 Db 11 RLQ 13

RESULT 12

A35105
 hypothetical protein - *Neurospora crassa* mitochondrion (fragment)
 C;Species: mitochondrion *Neurospora crassa*
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
 C;Accession: A35105
 R;Saville, B.J.; Collins, R.A.
 Cell 61, 685-696, 1990
 A;Title: A site-specific self-cleavage reaction performed by a novel RNA in *neurospora* mitochondria.
 A;Reference number: A35105; MUID:90263093; PMID:2160856
 A;Accession: A35105
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-14 <SAV>
 C;Genetics:
 A;Genome: mitochondrion
 A;Genetic code: SGC3
 C;Keywords: mitochondrion

Query Match 33.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQL 7
 |||
 Db 8 LQL 10

RESULT 13

I54284
 C1-inhibitor - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
 C;Accession: I54284

R;Siddique, Z.; McPhaden, A.R.; McCluskey, D.; Whaley, K.
Hum. Hered. 42, 231-234, 1992
A;Title: A single base deletion from the C1-inhibitor gene causes type I
hereditary angio-oedema.
A;Reference number: I54284; MUID:92380682; PMID:1339401
A;Accession: I54284
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14 <RES>
A;Cross-references: GB:S44615; NID:g254386; PIDN:AAB23055.1; PID:g254387

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LRC 9
|||
Db 5 LRC 7

RESULT 14

B61235
fibroblast-activating factor 35K precursor - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 12-May-1994
C;Accession: B61235
R;Demeter, J.; Medzihradzsky, D.; Kha, H.; Goetzl, E.J.; Turck, C.W.
Immunology 72, 350-354, 1991
A;Title: Isolation and partial characterization of the structures of fibroblast
activating factor-related proteins from U937 cells.
A;Reference number: A61235; MUID:91224664; PMID:2026444
A;Accession: B61235
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <DEM>

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQL 7
|||
Db 7 LQL 9

RESULT 15

A43847
Ig mu chain V region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 17-Apr-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: A43847; A37272
R;Dorward, D.W.; Huguenel, E.D.; Davis, G.; Garon, C.F.
Infect. Immun. 60, 838-844, 1992
A;Title: Interactions between extracellular *Borrelia burgdorferi* proteins and
non-*Borrelia*-directed immunoglobulin M antibodies.
A;Reference number: A43847; MUID:92175997; PMID:1541558
A;Accession: A43847

A;Molecule type: protein
A;Residues: 'Z',2-14 <DOR>
A;Note: sequence extracted from NCBI backbone (NCBIP:85360)
A;Note: the identifications of the protein and of the source were confirmed by the author
C;Keywords: immunoglobulin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
|||
Db 3 QLR 5

Search completed: November 13, 2003, 10:39:54
Job time : 8.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:55:06 ; Search time 4.875 Seconds
(without alignments)
86.819 Million cell updates/sec

Title: US-09-228-866-5
Perfect score: 9
Sequence: 1 CNSRLQLRC 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1246

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

No.	Score	Match	Length	DB	ID	Description
1	4	44.4	16	1	PA21_TRIST	P82892 trimeresuru
2	3	33.3	12	1	YZPY_ECOLI	P17776 escherichia
3	3	33.3	15	1	UC13_MAIZE	P80619 zea mays (m
4	3	33.3	15	1	UC27_MAIZE	P80633 zea mays (m
5	3	33.3	16	1	BRB_BASAL	P83187 basella alb
6	3	33.3	16	1	UVSX_BPT6	Q06728 bacterioph
7	3	33.3	20	1	CLPB_ACICA	P82956 acinetobact
8	3	33.3	20	1	OM4V_VIBAL	P83149 vibrio algi
9	2	22.2	7	1	CARP_MYTED	P10420 mytilus edu
10	2	22.2	7	1	CHOX_ALCSP	P16101 alcaligenes
11	2	22.2	7	1	FAR1_HELTI	P41871 helisoma tr
12	2	22.2	7	1	FAR1_MACRS	P83274 macrobrachi
13	2	22.2	7	1	FAR1_PROCL	P38499 procambarus
14	2	22.2	7	1	FAR2_ASCSU	P31890 ascaris suu
15	2	22.2	7	1	FAR2_PROCL	P38498 procambarus
16	2	22.2	8	1	AKH_MELML	P25423 melolontha
17	2	22.2	8	1	AKH_TABAT	P14595 tabanus atr
18	2	22.2	8	1	ALL3_CYDPO	P82154 cydia pomon
19	2	22.2	8	1	FAR1_PANRE	P41872 panagrellus
20	2	22.2	8	1	FAR1_PENMO	P83316 penaeus mon
21	2	22.2	8	1	FAR2_MACRS	P83275 macrobrachi
22	2	22.2	8	1	FAR3_HOMAM	P41486 homarus ame
23	2	22.2	8	1	FAR4_HOMAM	P41487 homarus ame
24	2	22.2	8	1	FAR4_MACRS	P83277 macrobrachi
25	2	22.2	8	1	HTF2_PERAM	P04549 periplaneta
26	2	22.2	8	1	HTF_TENMO	P25419 tenebrio mo
27	2	22.2	8	1	LCK1_LEUMA	P21140 leucophaea
28	2	22.2	8	1	LCK3_LEUMA	P21142 leucophaea
29	2	22.2	8	1	LMT2_LOCFI	P22396 locusta mig
30	2	22.2	8	1	LPK_LEUMA	P13049 leucophaea
31	2	22.2	8	1	LPMS_STAEP	P23211 staphylococ
32	2	22.2	8	1	PPK2_PERAM	P82692 periplaneta
33	2	22.2	8	1	PPK3_PERAM	P82618 periplaneta
34	2	22.2	8	1	RPCH_PANBO	P08939 pandalus bo
35	2	22.2	9	1	CCAP_CARMA	P38556 carcinus ma
36	2	22.2	9	1	FAR2_PANRE	P41873 panagrellus
37	2	22.2	9	1	FAR3_MACRS	P83276 macrobrachi
38	2	22.2	9	1	FAR3_PENMO	P83318 penaeus mon
39	2	22.2	9	1	FAR4_PENMO	P83319 penaeus mon
40	2	22.2	9	1	FAR5_PENMO	P83320 penaeus mon
41	2	22.2	9	1	FAR6_MACRS	P83279 macrobrachi
42	2	22.2	9	1	FAR8_MACRS	P83281 macrobrachi
43	2	22.2	9	1	FAR9_ASCSU	P43172 ascaris suu
44	2	22.2	9	1	FARP_CALSI	P38495 callinectes
45	2	22.2	9	1	HUTU_KLEAE	P12381 klebsiella

ALIGNMENTS

RESULT 1

PA21_TRIST

ID PA21_TRIST STANDARD; PRT; 16 AA.

AC P82892;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-I) (PLA2-I)
 DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
 OS Trimeresurus stejnegeri (Chinese green tree viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=39682;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Li S.Y., Wang W.Y., Xiong Y.L.;
 RT "Isolation, sequence and characterization of five variants of
 RT phospholipase A2 from venom of snake Trimeresurus stejnegeri."
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
 CC SUBFAMILY.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 2012 MW; 4EF2D4959E981117 CRC64;

Query Match 44.4%; Score 4; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQLR 8
 |||||
 Db 3 LQLR 6

RESULT 2

YZPY_ECOLI

ID YZPY_ECOLI STANDARD; PRT; 12 AA.
 AC P17776;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Hypothetical pyrE leader peptide.
 GN PYRL OR PYRE-LP.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85003588; PubMed=6207018;
 RA Poulsen P., Bonekamp F., Jensen K.F.;

RT "Structure of the Escherichia coli pyrE operon and control of pyrE
 RT expression by a UTP modulated intercistronic attenuation.";
 RL EMBO J. 3:1783-1790(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=83287414; PubMed=6349999;
 RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
 RA Lundberg L.G.;
 RT "Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA
 RT in front of the protein-coding region.";
 RL Eur. J. Biochem. 135:223-229(1983).
 CC -!- CAUTION: THIS SEQUENCE, ACCORDING TO THE ECOSEQ DATABASE (K. RUDD)
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 CC BE DELETED IN FUTURE RELEASES.
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 CC -----
 DR EMBL; X00781; -; NOT_ANNOTATED_CDS.
 DR EMBL; V01578; -; NOT_ANNOTATED_CDS.
 DR PIR; A30400; LFECPE.
 KW Hypothetical protein.
 SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRL 5
 |||
 Db 2 SRL 4

RESULT 3

UC13_MAIZE

ID UC13_MAIZE STANDARD; PRT; 15 AA.
 AC P80619;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.8, ITS MW IS: 56.9 kDa.
 CC -!- SIMILARITY: TO GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASES.
 DR Maize-2DPAGE; P80619; COLEOPTILE.
 DR MaizeDB; 123946; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQ 6
 |||
 Db 9 RLQ 11

RESULT 4

UC27_MAIZE

ID UC27 MAIZE STANDARD; PRT; 15 AA.
 AC P80633;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 688)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 48.4 kDa.
 CC -!- SIMILARITY: TO XENOPUS HISTONE-BINDING PROTEIN N1/N2 AND RABBIT
 CC AND HUMAN NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
 DR Maize-2DPAGE; P80633; COLEOPTILE.
 DR MaizeDB; 123958; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1853 MW; CA0E12A5DAED8DC7 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
 |||
Db 4 QLR 6

RESULT 5

BRB_BASAL

ID BRB_BASAL STANDARD; PRT; 16 AA.
AC P83187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-basrubin (Fragment).
OS Basella alba (Malabar spinach) (Ceylon spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Basellaceae; Basella.
OX NCBI_TaxID=3589;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21547763; PubMed=11688973;
RA Wang H., Ng T.B.;
RT "Novel antifungal peptides from ceylon spinach seeds."
RL Biochem. Biophys. Res. Commun. 288:765-770(2001).
CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,
CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.
CC Inhibits HIV-1 reverse transcriptase and cell-free translation.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.
KW Fungicide.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1952 MW; 28F9FE4FC181682C CRC64;

Query Match 33.3%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
 |||
Db 12 QLR 14

RESULT 6

UVSX_BPT6

ID UVSX_BPT6 STANDARD; PRT; 16 AA.
AC Q06728;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Recombination and repair protein (Fragment).
GN UVSX.
OS Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10666;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219141; PubMed=8464751;
 RA Winkler M., Rueger W.;
 RT "Cloning and sequencing of the genes of
 RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2
 RT and T6.";
 RL Nucleic Acids Res. 21:1500-1500(1993).
 CC -!- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND
 CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.
 CC INTERACTS WITH DDA AND GENE 32 PROTEINS.
 CC -!- SIMILARITY: Belongs to the recA family.
 CC -----
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 CC -----
 DR EMBL; X68725; CAA48668.1; -.
 DR PIR; S35627; S35627.
 KW DNA damage; DNA replication; DNA recombination; DNA repair;
 KW ATP-binding.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
 |||
 Db 8 SRL 10

RESULT 7

CLPB_ACICA

ID CLPB_ACICA STANDARD; PRT; 20 AA.
 AC P82956;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ClpB protein (Fragment).
 GN CLPB.
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=471;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=69-V;
 RX MEDLINE=21318969; PubMed=11425483;
 RA Benndorf D., Loffhagen N., Babel W.;
 RT "Protein synthesis patterns in Acinetobacter calcoaceticus induced by
 RT phenol and catechol show specificities of responses to chemostress.";

RL FEMS Microbiol. Lett. 200:247-252(2001).
 CC -!- SUBUNIT: Thought to be an ATPase subunit of an intracellular
 CC ATP-dependent protease (By similarity).
 CC -!- INDUCTION: By heat shock, primary alcohols and monocyclic
 CC aromatics, and weakly by catechol.
 CC -!- SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
 DR InterPro; IPR001270; Chaprnin_clpA/B.
 DR PROSITE; PS00870; CLPAB_1; PARTIAL.
 DR PROSITE; PS00871; CLPAB_2; PARTIAL.
 KW Chaperone; ATP-binding; Heat shock.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2320 MW; 86BC7F082D33E5BC CRC64;

Query Match 33.3%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RLQ 6
 |||
 Db 9 RLQ 11

RESULT 8

OM4V_VIBAL

ID OM4V_VIBAL STANDARD; PRT; 20 AA.
 AC P83149;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Outer membrane protein 40Va (Omp40Va) (Fragment).
 OS Vibrio alginolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=663;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 1903T;
 RA Onji M., Hirabayashi J., Suzuki S.;
 RT "Characterization of major outer membrane proteins of Vibrio
 RT alginolyticus and the stability against proteases."
 RL Microbes Environ. 0:0-0(2002).
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
 KW Transmembrane; Porin; Outer membrane.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2229 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 33.3%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLR 8
 |||
 Db 16 QLR 18

RESULT 9

CARP_MYTED

ID CARP_MYTED STANDARD; PRT; 7 AA.
 AC P10420;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Catch-relaxing peptide (CARP).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88052022; PubMed=3676797;
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.;
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
 CC RETRACTOR MUSCLE.
 DR PIR; A29342; ECMUCR.
 KW Hormone; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RL 5
 ||
 Db 6 RL 7

RESULT 10

CHOX_ALCSP

ID CHOX_ALCSP STANDARD; PRT; 7 AA.
 AC P16101;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Alcaligenes.
 OX NCBI_TaxID=512;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81006769; PubMed=6997283;
 RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 RT oxidase from Alcaligenes sp.";
 RL J. Biochem. 88:197-203(1980).
 CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
 DR PIR; A15398; A15398.
 KW Oxidoreductase.

FT NON_TER 7 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 6 SR 7

RESULT 11

FAR1_HELTI

ID FAR1_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LR 8
||
Db 5 LR 6

RESULT 12

FAR1_MACRS

ID FAR1_MACRS STANDARD; PRT; 7 AA.
AC P83274;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRFamide-like neuropeptide FLP1 (DRNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LR 8
 ||
 Db 5 LR 6

RESULT 13
 FAR1_PROCL
 ID FAR1_PROCL STANDARD; PRT; 7 AA.
 AC P38499;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog NF1.
 OS Procambarus clarkii (Red swamp crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procambarus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 RT pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LR 8
||
Db 5 LR 6

RESULT 14

FAR2_ASCSU

ID FAR2_ASCSU STANDARD; PRT; 7 AA.
AC P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253, 6233;
RN [1]
RP SEQUENCE.
RC SPECIES=A.suum;
RX MEDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL Peptides 14:423-430(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=P.redivivus;
RX MEDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the
RT free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RL Parasitology 109:351-356(1994).
CC -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LR 8
||
Db 5 LR 6

RESULT 15

FAR2_PROCL

ID FAR2_PROCL STANDARD; PRT; 7 AA.

AC P38498;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Cardioexcitatory FMRFamide homolog DF2.

OS Procamburus clarkii (Red swamp crayfish).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procamburus.

OX NCBI_TaxID=6728;

RN [1]

RP SEQUENCE.

RC TISSUE=Pericardial organs;

RX MEDLINE=93248032; PubMed=8387183;

RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;

RT "Isolation of two FMRFamide-related peptides from crayfish

RT pericardial organs.";

RL Peptides 14:137-143(1993).

CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS

CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF

CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 7 7 AMIDATION.

SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LR 8

||

Db 5 LR 6

Search completed: November 13, 2003, 10:33:58

Job time : 4.875 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:58:36 ; Search time 22.125 Seconds

(without alignments)

104.971 Million cell updates/sec

Title: US-09-228-866-5

Perfect score: 9

Sequence: 1 CNSRLQLRC 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7516

Minimum DB seq length: 7

Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	44.4	19	6	Q95J98	Q95j98 sus scrofa
2	4	44.4	19	10	Q9LGN8	Q9lgn8 oryza sativ
3	4	44.4	21	2	Q53014	Q53014 rhizobium e
4	3	33.3	8	2	P72279	P72279 rhodococcus
5	3	33.3	9	4	Q9UC36	Q9uc36 homo sapien
6	3	33.3	9	5	Q9TWD6	Q9twd6 leptinotars
7	3	33.3	9	11	Q9QWG2	Q9qwg2 mus musculu
8	3	33.3	10	4	Q9UN90	Q9un90 homo sapien
9	3	33.3	10	8	Q8SHG2	Q8shg2 chamaeleo j
10	3	33.3	10	15	Q8UT83	Q8ut83 human immun
11	3	33.3	11	2	Q9R7U8	Q9r7u8 pseudomonas
12	3	33.3	11	2	P77404	P77404 escherichia
13	3	33.3	11	4	Q8NFN9	Q8nfn9 homo sapien
14	3	33.3	11	15	Q98YS3	Q98ys3 human immun

15	3	33.3	11	15	Q83410	Q83410 mouse mamma
16	3	33.3	12	15	Q85631	Q85631 avian carci
17	3	33.3	12	16	O25179	O25179 helicobacte
18	3	33.3	13	6	Q9TRW6	Q9trw6 bos taurus
19	3	33.3	13	6	Q8WMM1	Q8wmm1 sus scrofa
20	3	33.3	13	15	Q85645	Q85645 mouse mamma
21	3	33.3	14	2	Q55326	Q55326 synechococc
22	3	33.3	14	2	Q9R5M2	Q9r5m2 borrelia bu
23	3	33.3	14	2	P83159	P83159 anabaena sp
24	3	33.3	14	4	Q99902	Q99902 homo sapien
25	3	33.3	14	4	O75692	O75692 homo sapien
26	3	33.3	14	11	Q9QV81	Q9qv81 rattus sp.
27	3	33.3	14	12	Q9PY99	Q9py99 murine hepa
28	3	33.3	14	15	Q8JDM3	Q8jdm3 human immun
29	3	33.3	14	15	Q8JDM7	Q8jdm7 human immun
30	3	33.3	14	15	Q8JDM0	Q8jdm0 human immun
31	3	33.3	15	2	Q9R545	Q9r545 mycobacteri
32	3	33.3	15	3	Q9UR64	Q9ur64 pleurotus o
33	3	33.3	15	3	Q9URE0	Q9ure0 saccharomyc
34	3	33.3	15	4	P78533	P78533 homo sapien
35	3	33.3	15	7	Q9TNQ1	Q9tnq1 mus sp. bet
36	3	33.3	15	10	Q9S8X0	Q9s8x0 nicotiana a
37	3	33.3	15	11	Q62544	Q62544 mus spretus
38	3	33.3	16	4	Q9UP51	Q9up51 homo sapien
39	3	33.3	16	4	Q9UCA6	Q9uca6 homo sapien
40	3	33.3	16	4	Q96RT5	Q96rt5 homo sapien
41	3	33.3	17	4	Q9HB76	Q9hb76 homo sapien
42	3	33.3	17	10	Q94FC0	Q94fc0 arabidopsis
43	3	33.3	17	12	Q64973	Q64973 alfalfa mos
44	3	33.3	17	12	Q64974	Q64974 alfalfa mos
45	3	33.3	18	2	Q9R5G0	Q9r5g0 alcaligenes

ALIGNMENTS

RESULT 1

Q95J98

ID Q95J98 PRELIMINARY; PRT; 19 AA.
AC Q95J98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Laminin gamma 1 chain (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiovascular;
RA Markmann A., Kresse H.;
RT "Regulation of VSMC Differentiation.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF330204; AAL09470.1; -.
FT NON_TER 1 1
FT NON_TER 19 19

SQ SEQUENCE 19 AA; 2214 MW; 8D3245EE2DD7EB6C CRC64;

Query Match 44.4%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
 ||||
Db 11 SRLQ 14

RESULT 2

Q9LGN8

ID Q9LGN8 PRELIMINARY; PRT; 19 AA.
AC Q9LGN8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0684C01.7 protein.
GN P0684C01.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:
RT P0684C01.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP002487; BAB07946.1; -.
DR Gramene; Q9LGN8; -.
SQ SEQUENCE 19 AA; 2160 MW; F0D8CA0C3BFEBB86 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQLR 8
 ||||
Db 15 LQLR 18

RESULT 3

Q53014

ID Q53014 PRELIMINARY; PRT; 21 AA.
AC Q53014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Nitrogenase alpha subunit (NifD) truncated (Fragment).
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CE-3;
 RX MEDLINE=96236026; PubMed=8655489;
 RA Valderrama B., Davalos A., Girard L., Morett E., Mora J.;
 RT "Regulatory proteins and cis-acting elements involved in the
 RT transcriptional control of Rhizobium etli reiterated nifH genes.";
 RL J. Bacteriol. 178:3119-3126(1996).
 DR EMBL; L13618; AAB07744.1; -.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2490 MW; 19282319A357D445 CRC64;

Query Match 44.4%; Score 4; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRLQ 6
 ||||
 Db 16 SRLQ 19

RESULT 4
 P72279

ID P72279 PRELIMINARY; PRT; 8 AA.
 AC P72279;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Biphenyl dioxygenase (Fragment).
 GN BPHB.
 OS Rhodococcus globerulus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.
 OX NCBI_TaxID=33008;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95255652; PubMed=7737502;
 RA Asturias J.A., Diaz E., Timmis K.N.;
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
 RT positive bacterium Rhodococcus globerulus P6 to multicomponent
 RT dioxygenases of gram-negative bacteria.";
 RL Gene 156:11-18(1995).
 DR EMBL; X80041; CAA56350.1; -.
 KW Dioxygenase.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQ 6
 |||
 Db 2 RLQ 4

RESULT 5

Q9UC36

ID Q9UC36 PRELIMINARY; PRT; 9 AA.
 AC Q9UC36;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92218434; PubMed=1560006;
 RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
 RT "Copurification of small heat shock protein with alpha B crystallin
 RT from human skeletal muscle."
 RL J. Biol. Chem. 267:7718-7725(1992).
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
 |||
 Db 6 SRL 8

RESULT 6

Q9TWD6

ID Q9TWD6 PRELIMINARY; PRT; 9 AA.
 AC Q9TWD6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE LED-NPF-1=NEUROPEPTIDE F-related peptide.
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96245438; PubMed=8814784;
 RA Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,
 RA Van Beeumen J., De Loof A.;
 RT "Insect neuropeptide F (NPF)-related peptides: isolation from Colorado
 RT potato beetle (Leptinotarsa decemlineata) brain."
 RL Insect Biochem. Mol. Biol. 26:375-382(1996).
 SQ SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;

Query Match 33.3%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
|||
Db 5 QLR 7

RESULT 7

Q9QWG2

ID Q9QWG2 PRELIMINARY; PRT; 9 AA.
AC Q9QWG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Protein G beta-2 subunit (Fragment).
GN GNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98030528; PubMed=9365246;
RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
RA Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IW32 cells is issued from a rearrangement between the
RT G-protein b2 gene subunit and the Epo genes.";
RL Oncogene 15:1995-1999(1997).
DR EMBL; Y11970; CAA72706.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1133 MW; 86FD0736DB172B05 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
|||
Db 6 QLR 8

RESULT 8

Q9UN90

ID Q9UN90 PRELIMINARY; PRT; 10 AA.
AC Q9UN90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Canalicular multispecific organic anion transporter (Fragment).
GN CMOAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Tanaka T., Uchiumi T., Hinoshita E., Inokuchi A., Toh S., Wada M.,
 RA Nomoto M., Kohno K., Kuwano M.;
 RT "Sequence analysis and functional characterization of the 5'-flanking
 RT region of the human canalicular multispecific organic anion
 RT transporter/multidrug resistance protein 2 (cMOAT/MRP2) gene.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF144630; AAD47599.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1219 MW; 76F28CB44EB9C33B CRC64;

Query Match 33.3%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNS 3
 |||
 Db 6 CNS 8

RESULT 9

Q8SHG2

ID Q8SHG2 PRELIMINARY; PRT; 10 AA.
 AC Q8SHG2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Chamaeleo jacksonii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBI_TaxID=116114;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 RT Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF448753; AAL90541.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1368 MW; C72180C733640736 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLR 8
 |||
 Db 3 QLR 5

RESULT 10

Q8UT83

ID Q8UT83 PRELIMINARY; PRT; 10 AA.
 AC Q8UT83;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Vpu protein.
 GN VPU.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=00BW1795.6;
 RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
 RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
 RA Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
 RA Marlink R., Lee T.-H., Essex M.;
 RT "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
 RT vaccine design.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF443097; AAL34766.1; -.
 SQ SEQUENCE 10 AA; 1264 MW; 91E52CB33321B37A CRC64;

Query Match 33.3%; Score 3; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
 |||
 Db 8 SRL 10

RESULT 11

Q9R7U8

ID Q9R7U8 PRELIMINARY; PRT; 11 AA.
 AC Q9R7U8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DNR protein (A regulatory protein for the expression of the Nir and
 DE nor genes) (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAO1;
 RX MEDLINE=95226457; PubMed=7711073;
 RA Arai H., Igarashi Y., Kodama T.;
 RT "The structural genes for nitric oxide reductase from Pseudomonas
 RT aeruginosa.";
 RL Biochim. Biophys. Acta 1261:279-284(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAO1;
 RX MEDLINE=95394152; PubMed=7664887;
 RA Arai H., Igarashi Y., Kodama T.;
 RT "Expression of the nir and nor genes for denitrification of

RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR."
RL FEBS Lett. 371:73-76(1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQL 7
|||
Db 3 LQL 5

RESULT 12

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.
AC P77404;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
GN HSDR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97206151; PubMed=9157244;
RA Tyndall C., Lehnher H., Sandmeier U., Kulik E., Bickle T.A.;
RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
RT high homology to the phage P1 genome: implications for the evolution
RT and spread of DNA restriction systems."
RL Mol. Microbiol. 23:729-736(1997).
DR EMBL; X98145; CAA66840.1; -.
DR EMBL; X98144; CAA66839.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRL 5
|||
Db 3 SRL 5

RESULT 13

Q8NFN9

ID Q8NFN9 PRELIMINARY; PRT; 11 AA.
AC Q8NFN9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Corticotropin releasing hormone receptor 1 (Fragment).
 GN CRHR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Parham K.L., Catalano R., Hillhouse E.W.;
 RT "Identification of the Promoter Region of the Human Type 1 CRH
 RT Receptor Gene.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF488558; AAM55213.1; -.
 KW Receptor.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1236 MW; ECEE030D0736C761 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
 |||
 Db 6 QLR 8

RESULT 14

Q98YS3

ID Q98YS3 PRELIMINARY; PRT; 11 AA.
 AC Q98YS3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN POL.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=985829;
 RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
 RA Korn K.;
 RT "Recovery of HIV-1 pol gene sequences by direct sequencing of
 RT amplification products derived from plasma samples.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF347394; AAK32471.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1195 MW; E96941B8D878773A CRC64;

Query Match 33.3%; Score 3; DB 15; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLR 8
 |||

Db

8 QLR 10

RESULT 15

Q83410

ID Q83410 PRELIMINARY; PRT; 11 AA.
AC Q83410;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Superantigen (Fragment).
GN SAG.
OS Mouse mammary tumor virus.
OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11757;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mtv-6;
RX MEDLINE=95133174; PubMed=7831795;
RA Cho K., Ferrick D.A., Morris D.W.;
RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
RT provirus.";
RL Virology 206:395-402(1995).
DR EMBL; L37518; AAA66963.1; -.
DR InterPro; IPR001213; MMTV_SAg.
DR Pfam; PF01054; MMTV_SAg; 1.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326C6D7 CRC64;

Query Match 33.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLQ 6
|||
Db 3 RLQ 5

Search completed: November 13, 2003, 10:38:13
Job time : 24.125 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 09:53:11 ; Search time 22.4583 Seconds
(without alignments)
49.473 Million cell updates/sec

Title: US-09-228-866-6
Perfect score: 7
Sequence: 1 CGVRLGC 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 358712

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					
No.	Score	Match	Length	DB	ID	Description
1	7	100.0	7	18	AAW13417	Brain homing pepti
2	7	100.0	7	21	AAB07392	Brain homing pepti
3	7	100.0	7	22	AAE11798	Phage peptide #6 t
4	7	100.0	7	23	AAU10709	Brain homing pepti
5	6	85.7	15	19	AAW82252	CTLA-4 immunomodul
6	6	85.7	15	21	AAB17070	CTLA4-mimetic pept
7	6	85.7	15	23	ABB73325	Exemplary pharmaco
8	5	71.4	9	23	ABJ04552	Bone marrow target
9	5	71.4	9	23	ABJ04604	Bone marrow target
10	5	71.4	9	23	ABG31126	Scrambled control
11	5	71.4	14	22	AAM00668	Human protein frag
12	4	57.1	7	19	AAW60410	Tumour homing pept
13	4	57.1	7	20	AAW93737	Mouse B16B15b mela
14	4	57.1	7	21	AAB21827	Murine melanoma ho
15	4	57.1	7	22	AAE06405	Tumour homing pept
16	4	57.1	7	23	AAE20047	Complement C1s cat
17	4	57.1	8	14	AAR36051	Hepatitis C virus
18	4	57.1	8	14	AAR36052	Hepatitis C virus
19	4	57.1	8	14	AAR36053	Hepatitis C virus
20	4	57.1	8	14	AAR36054	Hepatitis C virus
21	4	57.1	8	14	AAR36055	Hepatitis C virus
22	4	57.1	8	14	AAR51958	Lipopolysaccharide
23	4	57.1	8	19	AAW70551	Peptide 6 used dur
24	4	57.1	8	19	AAW64686	Human ADNF-III R1
25	4	57.1	8	21	AAB23476	Activity dependent
26	4	57.1	8	21	AAY71141	N-terminal peptide
27	4	57.1	8	22	AAB72337	Activity dependent
28	4	57.1	8	23	AAE20048	Complement C1s cat
29	4	57.1	8	24	ABP96638	G3BP-2 peptide fra
30	4	57.1	9	17	AAW49379	Human leucocyte an
31	4	57.1	9	21	AAAY86807	Telomerase peptide
32	4	57.1	9	22	ABB14387	Human C35 peptide
33	4	57.1	9	23	AAE20049	Complement C1s cat
34	4	57.1	9	24	ABR28610	Human cancer-relat
35	4	57.1	9	24	ABR28622	Human cancer-relat
36	4	57.1	9	24	ABR28856	Human cancer-relat
37	4	57.1	9	24	ABR28968	Human cancer-relat
38	4	57.1	9	24	ABR29158	Human cancer-relat
39	4	57.1	9	24	ABR29237	Human cancer-relat
40	4	57.1	9	24	ABR29362	Human cancer-relat
41	4	57.1	9	24	ABR29437	Human cancer-relat
42	4	57.1	9	24	ABR29443	Human cancer-relat
43	4	57.1	9	24	ABR29587	Human cancer-relat
44	4	57.1	9	24	ABR29623	Human cancer-relat
45	4	57.1	9	24	ABR29632	Human cancer-relat

ALIGNMENTS

RESULT 1

AAW13417

ID AAW13417 standard; Peptide; 7 AA.

XX

AC AAW13417;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;
KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in
PT vivo panning method, specifically to identify brain, kidney,
PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 14; Page 67; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing
CC peptide that was identified using a novel method for obtaining
CC molecules that home to a selected organ or tissue. This in vivo
CC panning method typically involves administering a phage display
CC library to a subject, and identifying expressed peptides which
CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
CC vascular tissue or tumour tissue. The isolated peptides (see
CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
CC labels to the selected organ/tissue (claimed) or to identify and/or
CC isolate target molecules (claimed). The peptides can be directly
CC identified in vivo, as compared to prior art in vitro screening
CC methods, which require further examination to see if they maintain
CC specificity in vivo.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGVRLGC 7

Db

|||||||
1 CGVRLGC 7

RESULT 2

AAB07392

ID AAB07392 standard; peptide; 7 AA.

XX

AC AAB07392;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 6.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..7

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in

PT vivo panning comprises administering a library of diverse peptides

PT linked to a tag which facilitates recovery of these peptides -

XX

PS Example 2; Column 17; 20pp; English.

XX

CC The present sequence is a mouse brain homing peptide. This sequence was

CC identified by using in vivo panning to screen a library of potential

CC organ homing molecules. The present sequence can be used to direct a

CC moiety to a the brain tissue, by linking the moiety to the present

CC sequence. Examples of potential moieties are drugs, toxins or a

CC detectable label. The present sequence contains a VRL amino acid motif.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CGVRLGC 7

Db

|||||||
1 CGVRLGC 7

RESULT 3

AAE11798

ID AAE11798 standard; peptide; 7 AA.

XX

AC AAE11798;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #6 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;

KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

FH Key Location/Qualifiers

FT Domain 3..5

FT /label= VLR_motif

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo

PT panning that selectively home to a selected organ or tissue useful for

PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGVRLGC 7
 |||||
Db 1 CGVRLGC 7

RESULT 4

AAU10709

ID AAU10709 standard; peptide; 7 AA.

XX

AC AAU10709;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #6 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;
KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.

XX

PT Recovering molecules that home to an organ or tissue, useful for
PT identifying molecules that home to a specific organ or tissue, e.g.
PT identifying a tumour homing molecule to identify the presence of cancer,
PT by in vivo panning of a library -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering
CC to the subject the library of diverse molecules, collecting a sample of
CC the selected organ or tissue (e.g. brain or kidney), and recovering from
CC the sample several molecules that home to the selected organ or tissue.
CC The method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety

CC (e.g. drug, toxin or detectable label) to the selected organ.
CC Specifically, the method is useful for identifying the presence of cancer
CC in a subject by linking an appropriate moiety to a tumour homing
CC molecule. The present method provides a direct means for identifying
CC molecules that specifically home to a selected organ and, therefore
CC provides a significant advantage over previous methods, which require
CC that a molecule identified using an in vitro screening method
CC subsequently be examined to determine if it maintains its specificity in
CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
CC the present invention.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGVRLGC 7
|||
Db 1 CGVRLGC 7

RESULT 5

AAW82252

ID AAW82252 standard; peptide; 15 AA.

XX

AC AAW82252;

XX

DT 23-FEB-1999 (first entry)

XX

DE CTLA-4 immunomodulatory peptide F6.

XX

KW Bacteriophage fd-tet; immunomodulatory molecule; T cell activation;
KW antigen presenting cell; auxiliary impulse signal conduction; CTLA-4;
KW monoclonal antibody; immune regulation.

XX

OS Synthetic.

XX

PN W09846739-A1.

XX

PD 22-OCT-1998.

XX

PF 23-JUL-1997; 97WO-JP02540.

XX

PR 16-APR-1997; 97JP-0115303.

XX

PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX

PI Sugimura K;

XX

DR WPI; 1998-568725/48.

XX

PT Immunomodulatory peptide(s) regulating activation of T-cells by
PT antigen presenting cells - have two cysteine residues at least six
PT residues apart, and affect auxiliary impulse signal conduction on
PT the T-cells and/or antigen presenting cells.

XX

PS Claim 10; Page 34; 54pp; Japanese.

XX

CC The present invention describes immunomodulatory peptides which regulate
CC the auxiliary impulse signal conduction on T cells and/or antigen
CC presenting cells by interacting with the molecules associated with
CC auxiliary impulse signal conduction on these cells. The peptides are
CC recognised by antibodies to the molecules associated with this signal
CC conduction, such as antibodies to CTLA-4, CD-28, CD-80 or CD-86. The
CC peptides contain a sequence having two cysteine residues at least six
CC residues apart. The peptides are identified by screening a phage random
CC peptide library (containing a random sequence of 8 or more amino acid
CC residues expressed on a coat protein) using an antibody to one of the
CC molecules involved in auxiliary impulse signal conduction (such as
CC CTLA-4). The peptides can be used as immunomodulators for the treatment
CC of disorders of immune regulation, and for the design and screening of
CC potential agonists, antagonists and receptors associated with auxiliary
CC impulse signal conduction. The present sequence represents a CTLA-4
CC immunomodulatory peptide from the present invention.

XX

SQ Sequence 15 AA;

Query Match 85.7%; Score 6; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLGC 7

|||||

Db 3 GVRLGC 8

RESULT 6

AAB17070

ID AAB17070 standard; Peptide; 15 AA.

XX

AC AAB17070;

XX

DT 31-OCT-2000 (first entry)

XX

DE CTLA4-mimetic peptide sequence SEQ ID NO:126.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX

OS Synthetic.

XX

PN WO200024782-A2.

XX

PD 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US25044.

XX

PR 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 39; Page 238; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 15 AA;

Query Match 85.7%; Score 6; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLGC 7
|||||
Db 3 GVRLGC 8

RESULT 7
ABB73325
ID ABB73325 standard; Peptide; 15 AA.
XX
AC ABB73325;
XX
DT 05-APR-2002 (first entry)
XX
DE Exemplary pharmacologically active peptide SEQ ID NO:126.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;

KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX

OS Synthetic.

XX

PN WO200183525-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14310.

XX

PR 03-MAY-2000; 2000US-0563286.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX

DR WPI; 2002-130313/17.

XX

PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX

PS Claim 39; Page 61; 176pp; English.

XX

CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX

SQ Sequence 15 AA;

Query Match 85.7%; Score 6; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLGC 7
 |||||
Db 3 GVRLGC 8

RESULT 8

ABJ04552

ID ABJ04552 standard; Peptide; 9 AA.

XX

AC ABJ04552;

XX

DT 24-OCT-2002 (first entry)

XX

DE Bone marrow targeting peptide 2.

XX

KW BRASIL; targeting peptide; bacterial infection;

KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;

KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;

KW viral infection; cardiovascular disease; degenerative disease.

XX

OS Unidentified.

XX

PN WO200220822-A2.

XX

PD 14-MAR-2002.

XX

PF 07-SEP-2001; 2001WO-US28124.

XX

PR 08-SEP-2000; 2000US-231266P.

PR 17-JAN-2001; 2001US-0765101.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Arap W, Pasqualini R;

XX

DR WPI; 2002-404697/43.

XX

PT Identification of targeting peptides that can be used to treat diseases
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT of Selective Ligands) method comprises a single differential
PT centrifugation step -

XX

PS Example 6; Page 79; 167pp; English.

XX

CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
CC of Selective Interactive Ligands) to obtain a targeting peptide. The
CC BRASIL method of the invention involves: exposing a target to a phage
CC display library in a first phase; exposing the first phase to a second
CC phase; and separating the phage bound to the target from unbound phage.
CC The BRASIL method of the invention allows cell phages to be separated
CC from the remaining unbound phage in a single differential centrifugation
CC step. When compared to conventional cell panning methods, the BRASIL
CC method shows a significant increase in recovery of specific phage and a

CC substantial decrease in background. The BRASIL method is useful for
CC identifying targeting peptides. The targeting peptides identified by the
CC method of the invention are useful for treating disease states, such as:
CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
CC disease; bacterial infection; viral infection; cardiovascular disease and
CC degenerative disease. The present amino acid sequence represents a
CC targeting peptide of the invention.

XX

SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VRLGC 7

|||||

Db 5 VRLGC 9

RESULT 9

ABJ04604

ID ABJ04604 standard; Peptide; 9 AA.

XX

AC ABJ04604;

XX

DT 24-OCT-2002 (first entry)

XX

DE Bone marrow targeting peptide 54.

XX

KW BRASIL; targeting peptide; bacterial infection;

KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;

KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;

KW viral infection; cardiovascular disease; degenerative disease.

XX

OS Unidentified.

XX

PN WO200220822-A2.

XX

PD 14-MAR-2002.

XX

PF 07-SEP-2001; 2001WO-US28124.

XX

PR 08-SEP-2000; 2000US-231266P.

PR 17-JAN-2001; 2001US-0765101.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Arap W, Pasqualini R;

XX

DR WPI; 2002-404697/43.

XX

PT Identification of targeting peptides that can be used to treat diseases

PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis

PT of Selective Ligands) method comprises a single differential

PT centrifugation step -

XX

PS Example 6; Page 80; 167pp; English.

XX
 CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase; and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRLGC 7
 |||||
 Db 5 VRLGC 9

RESULT 10

ABG31126

ID ABG31126 standard; peptide; 9 AA.

XX

AC ABG31126;

XX

DT 21-OCT-2002 (first entry)

XX

DE Scrambled control peptide for imaging probes.

XX

KW Chromophore; imaging probe; spacer; inflammation; rheumatoid arthritis;
 KW cancer; cardiovascular disease; atherosclerosis; dermatological disease;
 KW Kaposi's sarcoma; psoriasis; ophthalmic disease; diabetic retinopathy;
 KW infectious disease; immunological disease;
 KW acquired immunodeficiency syndrome; AIDS; neurodegenerative disease;
 KW Alzheimer's disease; bone-related disease; osteoporosis;
 KW environmental disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 8

FT /label= OTHER

FT /note= "Lys is covalently attached to an FITC

FT (fluorescein isothiocyanate) moiety"

FT Modified-site 9

FT /label= OTHER

FT /note= "Cys is amidated and covalently linked to a

FT QSY7 (not defined) moiety"
 XX
 PN WO200256670-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 07-JAN-2002; 2002WO-US00379.
 XX
 PR 05-JAN-2001; 2001US-260123P.
 PR 19-MAR-2001; 2001US-277352P.
 PR 09-NOV-2001; 2001US-0277352.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Weissleder R, Tung C, Mahmood U;
 XX
 DR WPI; 2002-590684/63.
 XX
 PT Activatable imaging probe for in vivo target optical imaging, has
 PT chromophore attachment moiety chemically linked to chromophores, so
 PT that upon activation of probe, optical properties of chromophores are
 PT altered -
 XX
 PS Example 9; Page 48; 69pp; English.
 XX
 CC The invention relates to an activatable imaging probe (I) (activated by
 CC phosphorylation, dephosphorylation, pH mediated cleavage, conformation
 CC change, enzyme-mediated splicing, enzyme-mediated transfer of the one
 CC or more chromophores, hybridisation of a nucleic acid sequence to a
 CC complementary target nucleic acid, binding of the probe to an analyte,
 CC chemical modification of the chromophore or binding of the probe to a
 CC receptor) comprises a chromophore attachment moiety (II) and one or
 CC more chromophores (III), where (III) is chemically linked to (II), so
 CC that upon activation of (I), the optical properties of (III) are
 CC altered. The probe is useful for in vivo optical imaging of a target in a
 CC subject, by delivering the probe to the subject, allowing adequate time
 CC for activation of the probe within the target, illuminating the target
 CC with light of a wavelength absorbable by the chromophores, detecting a
 CC signal emitted by the chromophores, optionally, repeating the steps at
 CC predetermined intervals to enable evaluation of the emitted signal of
 CC the chromophores in the subject over time, and forming an optical image
 CC from the emitted signal. The method is useful for detecting a disease
 CC e.g. inflammation (e.g. rheumatoid arthritis) cancer, cardiovascular
 CC disease (e.g. atherosclerosis), dermatological disease (e.g. Kaposi's
 CC sarcoma and psoriasis), ophthalmic disease (e.g. diabetic retinopathy),
 CC infectious disease, immunological diseases (e.g. acquired
 CC immunodeficiency syndrome, AIDS), neurodegenerative disease (e.g.
 CC Alzheimer's disease and bone-related disease (e.g. osteoporosis) in
 CC the subject, for characterising a phenotype or genotype of a disease in
 CC the subject and for characterising the severity of a disease. The
 CC probe is also useful in in vivo imaging for simultaneous imaging of one
 CC or more different targets in a subject, in an optical imaging method
 CC for assessing activity of an agent in a subject, by carrying out the
 CC above said method, administering the agent to the subjects and
 CC repeating the above said steps, and comparing the emitted signals and
 CC images over time or at a different agent dose to assess the activity of
 CC the agent. The probe is useful for determining the presence of a

CC composition (e.g. drug or a polypeptide expressed by a gene) in a
CC subject. The illumination and detecting processes are carried out using
CC endoscope, catheter, tomographic system, surgical goggles with attached
CC bandpass filters or an intraoperative microscope. The probe is useful for
CC assessing the effective dosage of an agent in a subject, in an optical
CC imaging method for guiding therapeutic interventions (e.g. surgical
CC interventions) in a subject such as mammal e.g. human or animal model of
CC a disease, and in in vitro optical imaging method for assessing the
CC activity of an agent in a sample. The present sequence is a
CC scrambled control peptide spacer.

XX

SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLG 6
|||
Db 1 GVRLG 5

RESULT 11

AAM00668

ID AAM00668 standard; Peptide; 14 AA.

XX

AC AAM00668;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human protein fragment SEQ ID NO: 1218.

XX

KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.

XX

OS Homo sapiens.

XX

PN WO200151670-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JAN-2001; 2001WO-US00322.

XX

PR 07-JAN-2000; 2000US-0174962.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX

DR WPI; 2001-451871/48.

DR N-PSDB; AAH89787.

XX

PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -

XX

PS Disclosure; Page 452; 475pp; English.

XX
 CC The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention.

XX
 SQ Sequence 14 AA;

Query Match 71.4%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLG 6
 |||||
 Db 5 GVRLG 9

RESULT 12

AAW60410

ID AAW60410 standard; peptide; 7 AA.

XX

AC AAW60410;

XX

DT 24-AUG-1998 (first entry)

XX

DE Tumour homing peptide of the invention.

XX

KW Tumour homing peptide; in vivo panning; murine melanoma; tumour.

XX

OS Synthetic.

XX

PN WO9810795-A2.

XX

PD 19-MAR-1998.

XX

PF 10-SEP-1997; 97WO-US16086.

XX

PR 10-SEP-1996; 96US-0710067.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1998-207151/18.

XX

PT Tumour homing molecules and their conjugates - useful for, e g.

PT directing linked moiety to tumour containing angiogenic vasculature

XX

PS Example 5; Page 80; 105pp; English.

XX

CC AAW60390-432 represent peptides recovered from mouse melaanomas.
 CC The peptides are tumour homing peptides, and are identified by in
 CC vivo panning. The in vivo panning comprises administering a library
 CC of diverse peptides to a subject having a tumour, collecting a sample of
 CC the tumour, identifying a peptide that homes to the tumour, collecting a
 CC sample of normal tissue corresponding to the tumour, and determining
 CC that the peptide that homes to the tumour is not present in the normal
 CC tissue. The tumour homing peptides can be linked to a moiety (e.g.
 CC doxorubicin), and used to direct the moiety to a tumour.
 XX
 SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
 ||||
 Db 3 GVRL 6

RESULT 13

AAW93737

ID AAW93737 standard; Peptide; 7 AA.

XX

AC AAW93737;

XX

DT 28-JUN-1999 (first entry)

XX

DE Mouse B16B15b melanoma derived tumour homing peptide 22.

XX

KW Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
 KW occlusive thrombus; murine.

XX

OS Mus sp.

XX

PN WO9913329-A1.

XX

PD 18-MAR-1999.

XX

PF 08-SEP-1998; 98WO-US18895.

XX

PR 25-AUG-1998; 98US-0139802.

PR 10-SEP-1997; 97US-0926914.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1999-215158/18.

XX

PT Identifying molecules that home to angiogenic vasculature used as
 PT targets for anticancer agents

XX
PS Example VI; Page 115; 180pp; English.

XX
CC This invention describes novel peptides which home to angiogenic
CC vasculature, specifically of a tumour and which have anti-tumour,
CC anti-inflammatory, anti-angiogenic and anti-arthritis activity. Such
CC molecules are identified by treating a purified NGR receptor with a test
CC compound and identifying compounds that bind specifically to the NGR
CC receptor. The peptides of the invention are inhibitors of angiogenesis
CC and can be used to produce conjugates for delivering agents to
CC angiogenic vasculature, particularly anticancer drugs or an imaging
CC agent, for diagnosis or prognosis. These conjugates may be directed to
CC non-tumour angiogenic vasculature, e.g. that present in inflammatory,
CC regenerating or wounded tissue, e.g. for treatment of macular
CC degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides
CC provide specific targeting to tumours, especially their supporting
CC vasculature, since the NGR receptor is exposed to the circulation only in
CC angiogenic vasculature. Precise targeting should reduce the systemic
CC toxicity of anticancer drugs in the conjugates. Complete killing of all
CC target cells may not be essential since partial denudation of endothelium
CC may result in an occlusive thrombus, and endothelial cells are unlikely
CC to become resistant to anticancer agents nor to lose the targeting
CC receptor. AAW93622-W93809 and AAW93843-44 are examples of tumour homing
CC peptides used in the invention.

XX
SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
 ||||
Db 3 GVRL 6

RESULT 14

AAB21827

ID AAB21827 standard; Peptide; 7 AA.

XX

AC AAB21827;

XX

DT 22-MAR-2001 (first entry)

XX

DE Murine melanoma homing peptide #22.

XX

KW Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; murine.

XX

OS Mus sp.

XX

PN WO200042973-A2.

XX

PD 27-JUL-2000.

XX

PF 21-JAN-2000; 2000WO-US01602.

XX

PR 22-JAN-1999; 99US-0235902.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;

XX

DR WPI; 2000-499174/44.

XX

PT Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT selectively homes to a mammalian cell type or tissue linked to an
PT antimicrobial peptide, useful for the treatment of prostate cancer -

XX

PS Example 8; Page 96; 118pp; English.

XX

CC The present invention relates to homing pro-apoptotic conjugates,
CC comprising of a tumour homing molecule that selectively homes to a
CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC homing pro-apoptotic conjugates are selectively internalised by the
CC mammalian cell type or tissue and exhibits high toxicity, especially to
CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC toxicity when not linked to the tumor homing molecule. The conjugates are
CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC prostate cancer or melanoma. The present sequence is a homing peptide
CC isolated in the present invention, which can be conjugated to an
CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC present invention.

XX

SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5

||||

Db 3 GVRL 6

RESULT 15

AAE06405

ID AAE06405 standard; peptide; 7 AA.

XX

AC AAE06405;

XX

DT 25-SEP-2001 (first entry)

XX

DE Tumour homing peptide #22 from mouse B16B15b melanoma.

XX

KW Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
KW antimicrobial peptide; prostate cancer; tumour homing molecule; mouse;
KW cytostatic.

XX

OS Mus sp.

XX

PN WO200153342-A1.

XX

PD 26-JUL-2001.

XX
 PF 16-JAN-2001; 2001WO-US01362.
 XX
 PR 21-JAN-2000; 2000US-0489582.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Ruoslahti EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
 XX
 DR WPI; 2001-451901/48.
 XX
 PT Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
 PT prostate cancer, comprises a prostate-homing peptide linked to an
 PT antimicrobial peptide -
 XX
 PS Example 8; Page 95; 176pp; English.
 XX
 CC The patent discloses novel chimeric prostate-homing pro-apoptotic
 CC peptide which comprises a prostate-homing peptide linked to an
 CC antimicrobial peptide, where the chimeric peptide is selectively
 CC internalised by and exhibits high toxicity to prostate tissue and
 CC where the antimicrobial peptide has low mammalian cell toxicity when
 CC not linked to prostate-homing peptide. The chimeric peptide is used
 CC to direct an antimicrobial peptide in vivo to a prostate cancer, to
 CC induce selective toxicity in vivo in a prostate cancer, and to treat
 CC a patient with prostate cancer. The present sequence is a tumour
 CC homing peptide from mouse B16B15b melanoma. This sequence is useful
 CC in the homing of pro-apoptotic conjugates of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
 ||||
 Db 3 GVRL 6

Search completed: November 13, 2003, 10:32:55
 Job time : 23.4583 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:38:27 ; Search time 13.7083 Seconds
 (without alignments)
 93.222 Million cell updates/sec

Title: US-09-228-866-6
 Perfect score: 7
 Sequence: 1 CGVRLGC 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 124183

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	
1	5	71.4	9	15	US-10-039-831-17	Sequence 17, Appl
2	4	57.1	7	9	US-09-765-086-127	Sequence 127, App
3	4	57.1	7	10	US-09-883-727A-100	Sequence 100, App
4	4	57.1	7	12	US-10-375-992-127	Sequence 127, App
5	4	57.1	7	15	US-10-264-374-127	Sequence 127, App
6	4	57.1	8	10	US-09-883-727A-101	Sequence 101, App
7	4	57.1	9	9	US-09-796-294-47	Sequence 47, Appl
8	4	57.1	9	10	US-09-883-727A-102	Sequence 102, App
9	4	57.1	9	10	US-09-824-787B-108	Sequence 108, App
10	4	57.1	9	12	US-10-461-787-47	Sequence 47, Appl
11	4	57.1	10	8	US-08-821-739A-63	Sequence 63, Appl
12	4	57.1	10	10	US-09-883-727A-103	Sequence 103, App
13	4	57.1	10	11	US-09-572-404B-903	Sequence 903, App
14	4	57.1	10	11	US-09-572-404B-925	Sequence 925, App

15	4	57.1	10	11	US-09-572-404B-929	Sequence 929, App
16	4	57.1	10	11	US-09-572-404B-935	Sequence 935, App
17	4	57.1	10	11	US-09-572-404B-937	Sequence 937, App
18	4	57.1	10	11	US-09-572-404B-977	Sequence 977, App
19	4	57.1	10	11	US-09-572-404B-983	Sequence 983, App
20	4	57.1	10	11	US-09-572-404B-2038	Sequence 2038, Ap
21	4	57.1	10	12	US-10-062-587-10	Sequence 10, Appl
22	4	57.1	10	12	US-09-573-822C-681	Sequence 681, App
23	4	57.1	11	9	US-09-823-649A-5	Sequence 5, Appli
24	4	57.1	11	9	US-09-823-649A-15	Sequence 15, Appl
25	4	57.1	11	9	US-09-823-649A-16	Sequence 16, Appl
26	4	57.1	11	10	US-09-883-727A-104	Sequence 104, App
27	4	57.1	12	9	US-09-796-294-14	Sequence 14, Appl
28	4	57.1	12	10	US-09-883-727A-105	Sequence 105, App
29	4	57.1	12	12	US-10-461-787-14	Sequence 14, Appl
30	4	57.1	13	10	US-09-883-727A-106	Sequence 106, App
31	4	57.1	14	10	US-09-883-727A-107	Sequence 107, App
32	4	57.1	15	10	US-09-883-727A-108	Sequence 108, App
33	4	57.1	16	7	US-08-736-019-121	Sequence 121, App
34	4	57.1	16	10	US-09-883-727A-109	Sequence 109, App
35	4	57.1	16	11	US-09-910-009A-170	Sequence 170, App
36	4	57.1	16	11	US-09-910-009A-171	Sequence 171, App
37	4	57.1	16	11	US-09-910-009A-172	Sequence 172, App
38	4	57.1	16	11	US-09-910-009A-441	Sequence 441, App
39	4	57.1	16	11	US-09-910-009A-442	Sequence 442, App
40	4	57.1	16	11	US-09-910-009A-443	Sequence 443, App
41	4	57.1	16	12	US-10-006-760-68	Sequence 68, Appl
42	4	57.1	17	10	US-09-883-727A-110	Sequence 110, App
43	4	57.1	17	15	US-10-327-514-18	Sequence 18, Appl
44	4	57.1	18	10	US-09-883-727A-111	Sequence 111, App
45	4	57.1	18	11	US-09-999-220B-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
 US-10-039-831-17
 ; Sequence 17, Application US/10039831
 ; Publication No. US20030044353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weissleder, Ralph
 ; APPLICANT: Tung, Ching-Hsuan
 ; APPLICANT: Mahmood, Umar
 ; TITLE OF INVENTION: ACTIVATABLE IMAGING PROBES
 ; FILE REFERENCE: 00786-572001
 ; CURRENT APPLICATION NUMBER: US/10/039,831
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: US 60/277,352
 ; PRIOR FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: US 60/260,123
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 9
 ; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-039-831-17

Query Match 71.4%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRLG 6
|||||
Db 1 GVRLG 5

RESULT 2

US-09-765-086-127
; Sequence 127, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-127

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
|||||
Db 3 GVRL 6

RESULT 3

US-09-883-727A-100
; Sequence 100, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.

```

; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; TITLE OF INVENTION: Complement C1s
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/09/883,727A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C1s catalytic site-directed moiety
US-09-883-727A-100

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Query Match          57.1%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 RLGC 7
        ||||
Db      2 RLGC 5

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RESULT 4

US-10-375-992-127

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; Sequence 127, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
;   APPLICANT: Ruoslahti, Erkki
;               Pasqualini, Renata
;   TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
;                       Derived Therefrom, and Methods of Using Same
;   NUMBER OF SEQUENCES: 199
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Campbell & Flores
;       STREET: 4370 La Jolla Village Drive, Suite 700
;       CITY: San Diego
;       STATE: California
;       COUNTRY: United States
;       ZIP: 92122
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/375,992
;       FILING DATE: 27-Feb-2003
;       CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/926,914
;       FILING DATE: 10-SEP-1997
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Campbell, Cathryn A.
;       REGISTRATION NUMBER: 31,815

```

```

; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 127:
US-10-375-992-127

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Query Match          57.1%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 GVRL 5
        ||||
Db      3 GVRL 6

```

RESULT 5

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US-10-264-374-127
; Sequence 127, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-127

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Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      2 GVRL 5

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Db |||||
 3 GVRL 6

RESULT 6

US-09-883-727A-101
; Sequence 101, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; TITLE OF INVENTION: Complement C1s
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/09/883,727A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C1s catalytic site-directed moiety
US-09-883-727A-101

Query Match 57.1%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RLGC 7
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Db 2 RLGC 5

RESULT 7

US-09-796-294-47
; Sequence 47, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 80-88 of the TADG-14 protein
US-09-796-294-47

Query Match 57.1%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRLG 6
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Db 2 VRLG 5

RESULT 8

US-09-883-727A-102
; Sequence 102, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; TITLE OF INVENTION: Complement C1s
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/09/883,727A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C1s catalytic site-directed moiety
US-09-883-727A-102

Query Match 57.1%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLGC 7
|||
Db 2 RLGC 5

RESULT 9

US-09-824-787B-108
; Sequence 108, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-108

Query Match 57.1%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
|||
Db 6 GVRL 9

RESULT 10

US-10-461-787-47
; Sequence 47, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. US20030199010A1e1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 80-88 of the TADG-14 protein
US-10-461-787-47

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRLG 6
|||
Db 2 VRLG 5

RESULT 11

US-08-821-739A-63
; Sequence 63, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.

```

; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-63

```

```

Query Match          57.1%; Score 4; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      2 GVRL 5
        ||||
Db      4 GVRL 7

```

```

RESULT 12
US-09-883-727A-103
; Sequence 103, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; TITLE OF INVENTION: Complement C1s
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/09/883,727A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 103

```


; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C1s catalytic site-directed moiety
US-09-883-727A-103

Query Match 57.1%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLGC 7
|||
Db 2 RLGC 5

RESULT 13

US-09-572-404B-903
; Sequence 903, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 903
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ADRBK1 OR GRK2 OR BARK1 OR BARK at
434-443 and may
; OTHER INFORMATION: interact with Sequence 904 in this patent.
US-09-572-404B-903

Query Match 57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLGC 7
|||
Db 3 RLGC 6

RESULT 14

US-09-572-404B-925
; Sequence 925, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 925
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ADRBK1 OR GRK2 OR BARK1 OR BARK at
435-444 and may
; OTHER INFORMATION: interact with Sequence 926 in this patent.
US-09-572-404B-925

Query Match 57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLGC 7
 ||||
Db 2 RLGC 5

RESULT 15

US-09-572-404B-929
; Sequence 929, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 929
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ADRBK1 OR GRK2 OR BARK1 OR BARK at
436-445 and may
; OTHER INFORMATION: interact with Sequence 930 in this patent.
US-09-572-404B-929

Query Match 57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLGC 7
 ||||
Db 1 RLGC 4

Search completed: November 13, 2003, 11:12:32
Job time : 13.7083 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:26:01 ; Search time 6.85417 Seconds
(without alignments)
98.215 Million cell updates/sec

Title: US-09-228-866-6
Perfect score: 7
Sequence: 1 CGVRLGC 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3752

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3	42.9	9	2	B39841	dextranucrase (EC
2	3	42.9	9	2	S78420	ribosomal protein
3	3	42.9	10	1	ECLQ1M	tachykinin I - mig
4	3	42.9	10	1	ECLQ3M	tachykinin III - m
5	3	42.9	10	1	ECLQ4M	tachykinin IV - mi
6	3	42.9	11	1	ECLQ2M	tachykinin II - mi
7	3	42.9	11	2	PT0217	T-cell receptor be
8	3	42.9	12	2	S49547	hypothetical prote
9	3	42.9	12	2	PH1581	Ig H chain V-D-J r
10	3	42.9	13	2	S32551	glutathione transf
11	3	42.9	13	2	PH1596	Ig H chain V-D-J r
12	3	42.9	14	1	BSTD	bombesin - fire-be
13	3	42.9	14	2	A32654	fibrinopeptide A -
14	3	42.9	14	2	PH0945	T-cell receptor be
15	3	42.9	15	2	JP0101	fibrinogen alpha c
16	3	42.9	15	2	I29501	fibrinopeptide A -

17	3	42.9	15	2	F29501	fibrinopeptide A -
18	3	42.9	15	2	D48394	major fat-globule
19	3	42.9	15	2	S36896	ribosomal protein
20	3	42.9	15	2	PH1342	Ig heavy chain DJ
21	3	42.9	15	2	S51735	T-cell receptor be
22	3	42.9	15	2	PH1616	Ig H chain V-D-J r
23	3	42.9	15	2	PH0770	T-cell receptor be
24	3	42.9	16	2	C28854	fibrinopeptide A -
25	3	42.9	16	2	A24180	fibrinogen alpha c
26	3	42.9	16	2	B24180	fibrinogen alpha c
27	3	42.9	16	2	A28854	fibrinopeptide A -
28	3	42.9	16	2	B28854	fibrinopeptide A -
29	3	42.9	16	2	A29501	fibrinopeptide A -
30	3	42.9	16	2	G29501	fibrinopeptide A -
31	3	42.9	16	2	H29501	fibrinopeptide A -
32	3	42.9	16	2	C61414	chymotrypsin (EC 3
33	3	42.9	16	2	PH1580	Ig H chain V-D-J r
34	3	42.9	16	2	S65430	pyrogallol hydroxy
35	3	42.9	17	2	E29501	fibrinopeptide A -
36	3	42.9	17	2	PH0082	neuroglian protein
37	3	42.9	17	2	B61414	chymotrypsin (EC 3
38	3	42.9	18	2	I55453	zinc finger homeod
39	3	42.9	18	2	A61577	24k serine protein
40	3	42.9	18	2	F49255	T-cell receptor be
41	3	42.9	19	2	B29501	fibrinopeptide A -
42	3	42.9	19	2	C29501	fibrinopeptide A -
43	3	42.9	19	2	A61144	probable flagellar
44	3	42.9	19	2	PH1360	Ig heavy chain DJ
45	3	42.9	20	2	S50741	probable trypsin i

ALIGNMENTS

RESULT 1

B39841

dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)

C;Species: Streptococcus sobrinus

C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Jun-1993

C;Accession: B39841

R;Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.

J. Biol. Chem. 266, 8916-8922, 1991

A;Title: Isolation and sequence of an active-site peptide containing a catalytic aspartic acid from two Streptococcus sobrinus alpha-glucosyltransferases.

A;Reference number: A39841; MUID:91224988; PMID:1827439

A;Accession: B39841

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <MOO>

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 42.9%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4

|||

Db

2 GVR 4

RESULT 2

S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78420

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78420

A;Molecule type: protein

A;Residues: 1-9 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L41

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6

|||

Db 6 RLG 8

RESULT 3

ECLQ1M

tachykinin I - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08265

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08265

A;Molecule type: protein

A;Residues: 1-10 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4

|||

Db 8 GVR 10

RESULT 4

ECLQ3M

tachykinin III - migratory locust

N;Alternate names: locustatachykinin III
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C;Accession: A60073
 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochansky, J.P.; Nachman, R.J.; De Loof, A.
 Regul. Pept. 31, 199-212, 1990
 A;Title: Locustatachykinin III and IV: two additional insect neuropeptides with homology to peptides of the vertebrate tachykinin family.
 A;Reference number: A60073; MUID:91219696; PMID:2132575
 A;Accession: A60073
 A;Molecule type: protein
 A;Residues: 1-10 <SCH>
 C;Superfamily: tachykinin
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F;10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVR 4
 |||
 Db 8 GVR 10

RESULT 5

ECLQ4M

tachykinin IV - migratory locust

N;Alternate names: locustatachykinin IV
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C;Accession: B60073
 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochansky, J.P.; Nachman, R.J.; De Loof, A.
 Regul. Pept. 31, 199-212, 1990
 A;Title: Locustatachykinin III and IV: two additional insect neuropeptides with homology to peptides of the vertebrate tachykinin family.
 A;Reference number: A60073; MUID:91219696; PMID:2132575
 A;Accession: B60073
 A;Molecule type: protein
 A;Residues: 1-10 <SCH>
 C;Superfamily: tachykinin
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F;10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVR 4
 |||
 Db 8 GVR 10

RESULT 6

ECLQ2M

tachykinin II - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995
 C;Accession: S08266
 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
 FEBS Lett. 261, 397-401, 1990
 A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
 homology to peptides of the vertebrate tachykinin family.
 A;Reference number: S08265; MUID:90184489; PMID:2311766
 A;Accession: S08266
 A;Molecule type: protein
 A;Residues: 1-11 <SCH>
 C;Superfamily: tachykinin
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 9 GVR 11

RESULT 7

PT0217
 T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C;Accession: PT0217
 R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not
 restricted in non-obese diabetic mice.
 A;Reference number: PT0209; MUID:91217621; PMID:1902501
 A;Accession: PT0217
 A;Molecule type: mRNA
 A;Residues: 1-11 <NAK>
 C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
 |||
 Db 4 RLG 6

RESULT 8

S49547
 hypothetical protein 2 (insertion sequence IS1110) - Mycobacterium avium
 C;Species: Mycobacterium avium
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999
 C;Accession: S49547
 R;Perez, M.H.; Fomukong, N.G.; Hellyer, T.; Brown, I.N.; Dale, J.W.

Mol. Microbiol. 12, 717-724, 1994
A;Title: Characterization of IS1110, a highly mobile genetic element from Mycobacterium avium.
A;Reference number: S49546; MUID:94328924; PMID:8052124
A;Accession: S49547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <PER>
A;Cross-references: EMBL:Z23003

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 7 RLG 9

RESULT 9

PH1581
Ig H chain V-D-J region (wild-type clone 4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1581
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1581
A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 5 RLG 7

RESULT 10

S32551
glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
C;Accession: S32551; S32550
R;Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A;Title: Glutathione S-transferases of mouse liver: sex-related differences in the expression of various isozymes.
A;Reference number: S32548; MUID:92256466; PMID:1581342

A;Accession: S32551
A;Molecule type: protein
A;Residues: 1-13 <SIN1>
A;Experimental source: female
A;Accession: S32550
A;Molecule type: protein
A;Residues: 1-13 <SIN2>
A;Experimental source: male
C;Keywords: transferase

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRL 5
|||
Db 8 VRL 10

RESULT 11

PH1596

Ig H chain V-D-J region (wild-type clone 303) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1596

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1596

A;Molecule type: DNA

A;Residues: 1-13 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 4 RLG 6

RESULT 12

BSTD

bombesin - fire-bellied toad

C;Species: Bombina bombina (fire-bellied toad)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01564

R;Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A;Title: Isolation and amino acid sequences of alytesin and bombesin, two analogous active tetradecapeptides from the skin of European discoglossid frogs.

A;Reference number: A01564; MUID:72163516; PMID:4537042

A;Accession: A01564
A;Molecule type: protein
A;Residues: 1-14 <ANA>
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide;
pyroglutamic acid; secretagogue; vasodilator
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 3 RLG 5

RESULT 13

A32654

fibrinopeptide A - beaded lizard

C;Species: Heloderma sp. (beaded lizard)

C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000

C;Accession: A32654

R;Blombaek, B.; Blombaek, M.; Hann, C.

unpublished results, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy
and Serotaxonomy, Hawkes, J.G., ed., pp.3-20, Academic Press, London and New
York, 1968

A;Reference number: A29501

A;Accession: A32654

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <BLO>

C;Superfamily: unassigned animal peptides

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 12 GVR 14

RESULT 14

PH0945

T-cell receptor beta chain V-D-J region (clone 16) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0945

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0945

A;Molecule type: mRNA

A;Residues: 1-14 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

A;Note: the authors translated the codon TTC for residue 11 as Ser

C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 6 RLG 8

RESULT 15

JP0101

fibrinogen alpha chain - duck (fragment)

N;Contains: fibrinopeptide A

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_change 26-Jan-1996

C;Accession: JP0101

R;Min, Y.; Ping, Z.; Yaoshi, Z.

Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985

A;Title: Purification and primary structures of duck fibrinopeptides A and B.

A;Reference number: A94238

A;Accession: JP0101

A;Molecule type: protein

A;Residues: 1-15 <MIN>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

C;Keywords: blood coagulation; plasma; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 13 GVR 15

Search completed: November 13, 2003, 10:39:55

Job time : 7.85417 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:55:06 ; Search time 3.79167 Seconds
(without alignments)
86.819 Million cell updates/sec

Title: US-09-228-866-6
Perfect score: 7
Sequence: 1 CGVRLGC 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1246

Minimum DB seq length: 7

Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3	42.9	9	1	BS43_SERPL	P83375 serratia pl
2	3	42.9	9	1	TKC1_CALVO	P41517 calliphora
3	3	42.9	9	1	TKL1_LOCM1	P16223 locusta mig
4	3	42.9	10	1	TKL2_LOCM1	P16224 locusta mig
5	3	42.9	10	1	TKL3_LOCM1	P30249 locusta mig
6	3	42.9	10	1	TKL4_LOCM1	P30250 locusta mig
7	3	42.9	10	1	TRP5_LEUMA	P81737 leucophaea
8	3	42.9	11	1	TKC2_CALVO	P41518 calliphora
9	3	42.9	12	1	CXL3_CONMR	P58809 conus marmo
10	3	42.9	13	1	FIBA_CAVPO	P14445 cavia porce
11	3	42.9	14	1	ALYT_ALYOB	P08944 alytes obst
12	3	42.9	14	1	FIBA_HORSE	P14452 equus cabal
13	3	42.9	15	1	FIBA_ANAPL	P12801 anas platyr
14	3	42.9	15	1	FIBA_SYNCA	P14463 syncerus ca
15	3	42.9	16	1	FIBA_CERSI	P14535 ceratotheri
16	3	42.9	16	1	FIBA_EQUAS	P14449 equus asinu
17	3	42.9	16	1	FIBA_FELCA	P14450 felis silve
18	3	42.9	16	1	FIBA_HYLLA	P14453 hylobates l
19	3	42.9	16	1	FIBA_MACFU	P12803 macaca fusc
20	3	42.9	16	1	FIBA_MANLE	P14455 mandrillus
21	3	42.9	16	1	FIBA_ODOHE	P14459 odocoileus
22	3	42.9	16	1	FIBA_TAPTE	P14536 tapirus ter
23	3	42.9	16	1	PGTL_PELAC	P80563 pelobacter
24	3	42.9	17	1	CXMA_CONPE	P58926 conus penna
25	3	42.9	17	1	CXMB_CONPE	P58927 conus penna
26	3	42.9	17	1	FIBA_PIG	P14460 sus scrofa
27	3	42.9	17	1	TRP2_LEUMA	P81733 leucophaea
28	3	42.9	18	1	FIBA_CAMDR	P14444 camelus dro
29	3	42.9	18	1	FIBA_LAMGL	P14454 lama glama
30	3	42.9	19	1	FIBA_BISBO	P14441 bison bonas
31	3	42.9	19	1	FIBA_BUBBU	P14442 bubalus bub

32	3	42.9	19	1	FIBA_CEREL	P14446	cervus elap
33	3	42.9	19	1	FIBA_CERNI	P14447	cervus nipp
34	3	42.9	19	1	FIBA_MUNMU	P14457	muntiacus m
35	3	42.9	19	1	FIBA_RANTA	P14462	rangifer ta
36	3	42.9	19	1	FIBA_SHEEP	P14451	ovis aries
37	3	42.9	19	1	FIBB_LAMGL	P14473	lama glama
38	3	42.9	19	1	UKA1_HUMAN	P31940	homo sapien
39	3	42.9	20	1	AROQ_AMEYE	P46380	amycolatops
40	3	42.9	20	1	UCRQ_EQUAR	P81247	equisetum a
41	3	42.9	21	1	FER_PYRWO	P81638	pyrococcus
42	2	28.6	7	1	BRHP_CONIM	P58803	conus imper
43	2	28.6	7	1	CARP_MYTED	P10420	mytilus edu
44	2	28.6	8	1	COW2_CONPU	P58785	conus purpu
45	2	28.6	8	1	FAR4_MACRS	P83277	macrobrachi

ALIGNMENTS

RESULT 1

BS43_SERPL

ID BS43_SERPL STANDARD; PRT; 9 AA.

AC P83375;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bacteriocin serracin P 43 kDa subunit (Fragment).

OS Serratia plymuthica.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Serratia.

OX NCBI_TaxID=82996;

RN [1]

RP SEQUENCE, AND FUNCTION.

RC STRAIN=J7;

RX MEDLINE=22293561; PubMed=12406768;

RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,

RA Van Beeumen J., Thonart P.;

RT "Characterization of serracin P, a phage-tail-like bacteriocin, and

RT its activity against Erwinia amylovora, the fire blight pathogen.";

RL Appl. Environ. Microbiol. 68:5704-5710(2002).

CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).

CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium

CC E.amylovora.

DR InterPro; IPR006498; Tail_tube.

DR Pfam; PF04985; Phage_tube; 1.

KW Antibiotic; Bacteriocin.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4

|||

Db 5 GVR 7

RESULT 2

TKC1_CALVO

ID TKC1_CALVO STANDARD; PRT; 9 AA.
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 7 GVR 9

RESULT 3

TKL1_LOCFI

ID TKL1_LOCFI STANDARD; PRT; 9 AA.
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 7 GVR 9

RESULT 4

TKL2_LOCM1

ID TKL2_LOCM1 STANDARD; PRT; 10 AA.
 AC P16224;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Locustatachykinin II (TK-II).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 8 GVR 10

RESULT 5

TKL3_LOCM1

ID TKL3_LOCM1 STANDARD; PRT; 10 AA.
AC P30249;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin III (TK-III).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family.";
RL Regul. Pept. 31:199-212(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; A60073; ECLQ3M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 8 GVR 10

RESULT 6

TKL4_LOCM1

ID TKL4_LOCM1 STANDARD; PRT; 10 AA.
AC P30250;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin IV (TK-IV).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;

RX MEDLINE=91219696; PubMed=2132575;
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
 RA de Loof A.;
 RT "Locustat tachykinin III and IV: two additional insect neuropeptides
 RT with homology to peptides of the vertebrate tachykinin family.";
 RL Regul. Pept. 31:199-212(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 DR PIR; B60073; ECLQ4M.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1040 MW; 9E52CD71E9C87735 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 8 GVR 10

RESULT 7

TRP5_LEUMA

ID TRP5_LEUMA STANDARD; PRT; 10 AA.
 AC P81737;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tachykinin-related peptide 5 (LemTRP 5).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Midgut;
 RX MEDLINE=97053012; PubMed=8897641;
 RA Muren J.E., Naessel D.R.;
 RT "Isolation of five tachykinin-related peptides from the midgut of
 RT the cockroach Leucophaea maderae: existence of N-terminally extended
 RT isoforms.";
 RL Regul. Pept. 65:185-196(1996).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Brain;
 RX MEDLINE=97269266; PubMed=9114447;
 RA Muren J.E., Naessel D.R.;
 RT "Seven tachykinin-related peptides isolated from the brain of the
 RT madeira cockroach; evidence for tissue-specific expression of
 RT isoforms.";
 RL Peptides 18:7-15(1997).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
 CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: MIDGUT AND BRAIN.
 CC -!- MASS SPECTROMETRY: MW=1033.2; METHOD=MALDI.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 8 GVR 10

RESULT 8

TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
 AC P41518;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins."
 RL Peptides 15:761-768(1994).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 9 GVR 11

RESULT 9

CXL3_CONMR

ID CXL3_CONMR STANDARD; PRT; 12 AA.
 AC P58809;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrX.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1262.77; MW_ERR=0.07; METHOD=Electrospray.
 CC -!- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 3 12
 FT DISULFID 4 9
 FT MOD_RES 11 11 HYDROXYLATION.
 SQ SEQUENCE 12 AA; 1251 MW; 277AAE2422D5A2C8 CRC64;

 Query Match 42.9%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CGV 3
 |||
 Db 4 CGV 6

RESULT 10
 FIBA_CAVPO
 ID FIBA_CAVPO STANDARD; PRT; 13 AA.
 AC P14445;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 13 FIBRINOPEPTIDE A.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1309 MW; 639999286C79DDDB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 11 GVR 13

RESULT 11

ALYT_ALYOB

ID AYT_ALYOB STANDARD; PRT; 14 AA.
 AC P08944;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alytesin.
 OS Alytes obstetricans (Midwife toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.
 OX NCBI_TaxID=8443;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RT "Active peptides in the skins of one hundred amphibian species from
 RT Australia and Papua New Guinea.";
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 3 RLG 5

RESULT 12

FIBA_HORSE

ID FIBA_HORSE STANDARD; PRT; 14 AA.
AC P14452;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 12 GVR 14

RESULT 13

FIBA_ANAPL

ID FIBA_ANAPL STANDARD; PRT; 15 AA.
AC P12801;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS *Anas platyrhynchos* (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; *Anas*.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85168193; PubMed=3983613;
 RA Min Y., Ping Z., Yaoshi Z.;
 RT "Purification and primary structures of duck fibrinopeptides A and
 RT B.";
 RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR; JP0101; JP0101.
 KW Blood coagulation; Plasma; Pyrrolidone carboxylic acid.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1580 MW; D78A51FF88B40373 CRC64;

 Query Match 42.9%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 13 GVR 15

RESULT 14

FIBA_SYNCA

ID FIBA_SYNCA STANDARD; PRT; 15 AA.
 AC P14463;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS *Syncerus caffer* (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; *Syncerus*.
 OX NCBI_TaxID=9970;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67209145; PubMed=6033721;
 RA Doolittle R.F., Schubert D., Schwartz S.A.;

RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 RT Dromedary camel, mule deer, and cape buffalo.";
 RL Arch. Biochem. Biophys. 118:456-467(1967).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 13 GVR 15

RESULT 15

FIBA_CERSI

ID FIBA_CERSI STANDARD; PRT; 16 AA.
 AC P14535;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 OX NCBI_TaxID=9807;
 RN [1]
 RP SEQUENCE.
 RA O'Neil P.B., Doolittle R.F.;
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
 RL Syst. Zool. 22:590-595(1973).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 14 GVR 16

Search completed: November 13, 2003, 10:33:59
Job time : 4.79167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:58:36 ; Search time 17.2083 Seconds
(without alignments)
104.971 Million cell updates/sec

Title: US-09-228-866-6
Perfect score: 7
Sequence: 1 CGVRLGC 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7516

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*

16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	4	57.1	21	12	Q85616	Q85616 reovirus (t	
2	3	42.9	10	6	Q8SPN8	Q8spn8 macaca mula	
3	3	42.9	10	12	Q69347	Q69347 herpes simp	
4	3	42.9	11	2	Q9X9S6	Q9x9s6 streptomyce	
5	3	42.9	11	11	P97330	P97330 mus musculu	
6	3	42.9	11	12	Q8JS92	Q8js92 hepatitis b	
7	3	42.9	12	2	Q50959	Q50959 neisseria g	
8	3	42.9	12	2	P95606	P95606 alcaligenes	
9	3	42.9	13	4	Q9UPE6	Q9upe6 homo sapien	
10	3	42.9	13	6	Q9TUD7	Q9tud7 bos taurus	
11	3	42.9	14	2	P83159	P83159 anabaena sp	
12	3	42.9	14	4	Q8WWR7	Q8wwr7 homo sapien	
13	3	42.9	14	5	Q9TWW0	Q9tww0 trypanosoma	
14	3	42.9	14	13	Q8AXQ7	Q8axq7 xenopus lae	
15	3	42.9	15	2	Q9R544	Q9r544 mycobacteri	
16	3	42.9	15	6	Q8MIG5	Q8mig5 cynocephalu	
17	3	42.9	15	6	Q9TRG9	Q9trg9 bos taurus	
18	3	42.9	15	6	Q8MI95	Q8mi95 tupaia tana	
19	3	42.9	15	11	Q8K1W5	Q8klw5 castor cana	
20	3	42.9	16	2	Q9F1S7	Q9f1s7 streptococc	
21	3	42.9	16	2	Q9F1R9	Q9f1r9 streptococc	
22	3	42.9	16	2	Q9F1S4	Q9f1s4 streptococc	
23	3	42.9	16	2	Q9F1S1	Q9f1s1 streptococc	
24	3	42.9	16	8	Q9T2V8	Q9t2v8 homo sapien	
25	3	42.9	17	2	Q9R505	Q9r505 bacillus su	
26	3	42.9	17	2	Q9R4H9	Q9r4h9 bordetella	
27	3	42.9	17	3	Q8J167	Q8j167 hypocrea li	
28	3	42.9	17	6	Q8MIC8	Q8mic8 orycteropus	
29	3	42.9	17	6	Q8MIH7	Q8mih7 cyclopes di	
30	3	42.9	17	6	Q8MI97	Q8mi97 trichechus	
31	3	42.9	17	6	Q8MIF2	Q8mif2 elephas max	
32	3	42.9	17	6	Q8MIG7	Q8mig7 chrysochlor	
33	3	42.9	18	4	Q15912	Q15912 homo sapien	
34	3	42.9	18	5	Q9TWV6	Q9twv6 aplysia cal	
35	3	42.9	18	12	Q9DSS9	Q9dss9 human adeno	
36	3	42.9	18	12	Q9W9C1	Q9w9c1 human adeno	
37	3	42.9	18	15	O12692	O12692 simian-huma	
38	3	42.9	19	2	Q53545	Q53545 shigella so	
39	3	42.9	19	12	Q69345	Q69345 human herpe	
40	3	42.9	19	15	Q905K7	Q905k7 human immun	
41	3	42.9	20	2	Q51558	Q51558 pseudomonas	
42	3	42.9	20	2	Q9R4N1	Q9r4n1 rhodococcus	
43	3	42.9	20	10	Q9S8K2	Q9s8k2 solanum tub	
44	3	42.9	20	11	Q8VIL9	Q8vil9 mus musculu	
45	3	42.9	20	12	Q9PXE4	Q9pxe4 foot-and-mo	

ALIGNMENTS

RESULT 1

Q85616

ID Q85616 PRELIMINARY; PRT; 21 AA.
 AC Q85616;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Reovirus serotype 3 L2 (Fragment).
 OS Reovirus (type 3 / strain Dearing).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
 RT "Sequences at both termini of the 10 genes of reovirus serotype 3
 RT (strain Dearing).";
 RL Virology 121:307-319(1982).
 DR EMBL; J02315; AAA47270.1; -.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2304 MW; 277FBC9FC34D9D7C CRC64;

Query Match 57.1%; Score 4; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVRL 5
 ||||
 Db 6 GVRL 9

RESULT 2

Q8SPN8

ID Q8SPN8 PRELIMINARY; PRT; 10 AA.
 AC Q8SPN8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Solute carrier family 6 member 4 (Fragment).
 GN SLC6A4.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Norgren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
 RT "Construction of a targeted rhesus macaque microarray.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY083583; AAM11998.1; -.
 FT NON_TER 1 1

SQ SEQUENCE 10 AA; 1043 MW; 3B07C4473412CAA8 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRL 5
|||
Db 5 VRL 7

RESULT 3

Q69347

ID Q69347 PRELIMINARY; PRT; 10 AA.
AC Q69347;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.1 kDa protein.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KOS;
RX MEDLINE=86068025; PubMed=2999787;
RA Gibbs J.S., Chiou H.C., Hall J.D., Mount D.W., Retondo M.J.,
RA Weller S.K., Coen D.M.;
RT "Sequence and mapping analyses of the herpes simplex virus DNA
RT polymerase gene predict a C-terminal substrate binding domain."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7969-7973 (1985).
DR EMBL; M10792; AAA66437.1; -.
KW Hypothetical protein.
SQ SEQUENCE 10 AA; 1057 MW; C45DF17735BDC40D CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 8 GVR 10

RESULT 4

Q9X9S6

ID Q9X9S6 PRELIMINARY; PRT; 11 AA.
AC Q9X9S6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.2 kDa protein (Fragment).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TK21;
 RX MEDLINE=99328982; PubMed=10400594;
 RA Martinez-Costa O.H., Martin-Triana A.J., Martinez E.,
 RA Fernandez-Moreno M.A., Malpartida F.;
 RT "An additinal regulatory gene for actinorhodin production in
 RT Streptomyces lividans involves a LysR-type transcriptional
 RT regulator.";
 RL J. Bacteriol. 181:4353-4364(1999).
 DR EMBL; Y18818; CAB51138.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1160 MW; D1BABA8EC1EDC412 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 3 GVR 5

RESULT 5
 P97330

ID P97330 PRELIMINARY; PRT; 11 AA.
 AC P97330;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CD45-AP (LSM-1).
 GN PTPRCAP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97124850; PubMed=8954783;
 RA Bruyns E., Mincheva A., Bruyns R.M., Kirchgessner H., Weitz S.,
 RA Lichter P., Meuer S., Schraven B.;
 RT "Sequence, genomic organization and chromosomal Localization of the
 RT human LPAP (PTPRCAP) and Mouse CD45-AP/LSM-1 genes.";
 RL Genomics 38:79-83(1996).
 DR EMBL; X97268; CAA65923.1; -.
 DR MGD; MGI:97811; Ptprcap.
 SQ SEQUENCE 11 AA; 1150 MW; 50695413B5A772C7 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGC 7
 |||
 Db 9 LGC 11

RESULT 6

Q8JS92

ID Q8JS92 PRELIMINARY; PRT; 11 AA.
AC Q8JS92;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=34;
RX PubMed=12185284;
RA Hou J., Lin Y., Waters J., Wang Z., Min J., Liao H., Jiang J.,
RA Chen J., Luo K., Karayiannis P.;
RT "Detection and significance of a G1862T variant of hepatitis B virus
RT in Chinese patients with fulminant hepatitis.";
RL J. Gen. Virol. 83:2291-2298(2002).
DR EMBL; AF495695; AAM34089.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1315 MW; DC70528AB5B73412 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRL 5
|||
Db 4 VRL 6

RESULT 7

Q50959

ID Q50959 PRELIMINARY; PRT; 12 AA.
AC Q50959;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OpaE1 gene product (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11A;
RX MEDLINE=89210824; PubMed=2854063;
RA Taha M.K., So M., Seifert H.S., Billyard E., Marchal C.;
RT "Pilin expression in Neisseria gonorrhoeae is under both positive and
RT negative transcriptional control.";
RL EMBO J. 7:4367-4378(1988).
DR EMBL; X13965; CAB37342.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1436 MW; 9684516C16C87735 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 7 GVR 9

RESULT 8

P95606

ID P95606 PRELIMINARY; PRT; 12 AA.
AC P95606;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Nickel permease (Fragment).
GN HOXN.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16;
RX MEDLINE=91131629; PubMed=1847142;
RA Eitinger T., Friedrich B.;
RT "Cloning, nucleotide sequence, and heterologous expression of a high-
RT affinity nickel transport gene from Alcaligenes eutrophus.";
RL J. Biol. Chem. 266:3222-3227(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H16;
RA Lenz O.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U82564; AAB49367.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1367 MW; 478C45052BC87DD7 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
|||
Db 7 GVR 9

RESULT 9

Q9UPE6

ID Q9UPE6 PRELIMINARY; PRT; 13 AA.
AC Q9UPE6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).

GN IMPA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder.";
 RL Mol. Psychiatry 2:393-397(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20284187;
 RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
 RA Esterling L.E., Detera-Wadleigh S.D.;
 RT "Genomic structure and novel variants of myo-inositol monophosphatase
 RT 2.";
 RL Mol. Psychiatry 5:165-171(2000).
 DR EMBL; AF025884; AAD22137.1; -.
 DR EMBL; AF025883; AAD22137.1; JOINED.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1345 MW; FDE5871CE26EC871 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GVR 4
 |||
 Db 7 GVR 9

RESULT 10

Q9TUD7
 ID Q9TUD7 PRELIMINARY; PRT; 13 AA.
 AC Q9TUD7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Tie-2/tek receptor tyrosine kinase (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RA Hewett P.W., Daft E.L., Murray J.C.;
 RT "Cloning and characterisation of human tie-2/tek promoter.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF077857; AAF01566.1; -.
 KW Kinase; Receptor.

FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1295 MW; 8AF9F2F5BC0BC735 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGV 3
|||
Db 10 CGV 12

RESULT 11

P83159

ID P83159 PRELIMINARY; PRT; 14 AA.
AC P83159;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
DE rod (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS
CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
KW Phycobilisome; Photosynthesis.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1405 MW; 96823E44F60A3115 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
|||
Db 8 RLG 10

RESULT 12

Q8WWR7

ID Q8WWR7 PRELIMINARY; PRT; 14 AA.
AC Q8WWR7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Desmoglein 2 (Fragment).

GN DSG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tian Q., Schmidt A., Langbein L., Moll R., Franke W.W.;
 RT "Desmoglein 2."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ278448; CAC81989.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1726 MW; 6934FD64ED6E2BD4 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRL 5
 |||
 Db 8 VRL 10

RESULT 13

Q9TWW0
 ID Q9TWW0 PRELIMINARY; PRT; 14 AA.
 AC Q9TWW0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Histone C (Fragment).
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93064852; PubMed=1437281;
 RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
 RT "Sequence differences between histones of procyclic Trypanosoma brucei
 RT brucei and higher eukaryotes."
 RL Parasitology 105:97-104(1992).
 SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRL 5
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 Db 5 VRL 7

RESULT 14

Q8AXQ7
 ID Q8AXQ7 PRELIMINARY; PRT; 14 AA.
 AC Q8AXQ7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mannose-binding lectin-associated serine protease (Fragment).
 GN MASP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT "Ancient origin and extensive distribution of mannose-binding lectin-
 RT associated serine protease-3 in vertebrate lineage."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB078909; BAC41345.1; -.
 KW Lectin; Protease.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1533 MW; 99DDD285F40C2B15 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGV 3
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 Db 1 CGV 3

RESULT 15

Q9R544

ID Q9R544 PRELIMINARY; PRT; 15 AA.
 AC Q9R544;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 30S ribosomal protein S16 homolog (Fragment).
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94009653; PubMed=8405418;
 RA Ohara N., Kimura M., Higashi Y., Yamada T.;
 RT "Isolation and amino acid sequence of the 30S ribosomal protein S19
 RT from Mycobacterium bovis BCG."
 RL FEBS Lett. 331:9-14(1993).
 DR InterPro; IPR000307; Ribosomal_S16.
 DR PROSITE; PS00732; RIBOSOMAL_S16; 1.
 SQ SEQUENCE 15 AA; 1707 MW; 6D3E70FD26DDA931 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLG 6
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Db 8 RLG 10

Search completed: November 13, 2003, 10:38:14
Job time : 18.2083 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:27:36 ; Search time 9 Seconds
 (without alignments)
 37.610 Million cell updates/sec

Title: US-09-228-866-7
 Perfect score: 8
 Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 118358

Minimum DB seq length: 7
 Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	8	100.0	8	1	US-08-526-710-7 Sequence 7, Appli
2	8	100.0	8	3	US-08-862-855-7 Sequence 7, Appli
3	8	100.0	8	3	US-09-226-985-7 Sequence 7, Appli
4	8	100.0	8	4	US-09-227-906-7 Sequence 7, Appli
5	6	75.0	8	1	US-08-526-710-8 Sequence 8, Appli
6	6	75.0	8	3	US-08-862-855-8 Sequence 8, Appli
7	6	75.0	8	3	US-09-226-985-8 Sequence 8, Appli
8	6	75.0	8	4	US-09-227-906-8 Sequence 8, Appli
9	5	62.5	10	2	US-08-733-505A-35 Sequence 35, Appl
10	5	62.5	10	2	US-08-706-741B-70 Sequence 70, Appl
11	5	62.5	10	2	US-08-924-695A-70 Sequence 70, Appl

12	5	62.5	20	1	US-08-248-819A-39	Sequence 39, Appl
13	5	62.5	20	2	US-08-337-646A-57	Sequence 57, Appl
14	5	62.5	20	3	US-08-927-326-57	Sequence 57, Appl
15	5	62.5	21	1	US-08-112-208C-15	Sequence 15, Appl
16	5	62.5	21	1	US-08-248-819A-17	Sequence 17, Appl
17	5	62.5	21	2	US-08-337-646A-35	Sequence 35, Appl
18	5	62.5	21	2	US-08-856-531-15	Sequence 15, Appl
19	5	62.5	21	2	US-08-856-034-15	Sequence 15, Appl
20	5	62.5	21	3	US-08-927-326-35	Sequence 35, Appl
21	5	62.5	21	4	US-09-379-820A-15	Sequence 15, Appl
22	4	50.0	7	1	US-08-798-897-9	Sequence 9, Appli
23	4	50.0	7	2	US-08-978-523-9	Sequence 9, Appli
24	4	50.0	7	4	US-09-463-129B-6	Sequence 6, Appli
25	4	50.0	8	1	US-08-471-058-1	Sequence 1, Appli
26	4	50.0	8	3	US-08-471-057-1	Sequence 1, Appli
27	4	50.0	8	4	US-08-470-865-1	Sequence 1, Appli
28	4	50.0	10	2	US-08-733-505A-27	Sequence 27, Appl
29	4	50.0	10	2	US-08-733-505A-29	Sequence 29, Appl
30	4	50.0	10	2	US-08-706-741B-62	Sequence 62, Appl
31	4	50.0	10	2	US-08-706-741B-64	Sequence 64, Appl
32	4	50.0	10	2	US-08-924-695A-62	Sequence 62, Appl
33	4	50.0	10	2	US-08-924-695A-64	Sequence 64, Appl
34	4	50.0	11	2	US-08-733-505A-31	Sequence 31, Appl
35	4	50.0	11	2	US-08-733-505A-33	Sequence 33, Appl
36	4	50.0	11	2	US-08-706-741B-66	Sequence 66, Appl
37	4	50.0	11	2	US-08-706-741B-68	Sequence 68, Appl
38	4	50.0	11	2	US-08-924-695A-66	Sequence 66, Appl
39	4	50.0	11	2	US-08-924-695A-68	Sequence 68, Appl
40	4	50.0	13	1	US-08-248-819A-42	Sequence 42, Appl
41	4	50.0	13	1	US-08-248-819A-43	Sequence 43, Appl
42	4	50.0	13	1	US-08-798-897-30	Sequence 30, Appl
43	4	50.0	13	1	US-08-798-897-33	Sequence 33, Appl
44	4	50.0	13	2	US-08-337-646A-60	Sequence 60, Appl
45	4	50.0	13	2	US-08-337-646A-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1

US-08-526-710-7

; Sequence 7, Application US/08526710

; Patent No. 5622699

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Method of Identifying Molecules That

; TITLE OF INVENTION: Home to a Selected Organ In Vivo

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-7

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Query Match          100.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 CKDWGRIC 8
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Db      1 CKDWGRIC 8

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RESULT 2

US-08-862-855-7

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; Sequence 7, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-7

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Query Match          100.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CKDWGRIC 8
        |||||
Db      1 CKDWGRIC 8

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RESULT 3
US-09-226-985-7
; Sequence 7, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-7

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Query Match          100.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 CKDWGRIC 8
        |||||
Db      1 CKDWGRIC 8

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RESULT 4

US-09-227-906-7

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; Sequence 7, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-7

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Query Match          100.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 CKDWGRIC 8
        |||||
Db      1 CKDWGRIC 8

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RESULT 5

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US-08-526-710-8
; Sequence 8, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-8

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Query Match          75.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 DWGRIC 8
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Db      3 DWGRIC 8

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RESULT 6

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US-08-862-855-8
; Sequence 8, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-8

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Query Match          75.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      3 DWGRIC 8
        |||||
Db      3 DWGRIC 8

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RESULT 7

US-09-226-985-8

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; Sequence 8, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-8

```

```

Query Match          75.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 DWGRIC 8
        |||||
Db      3 DWGRIC 8

```

```

RESULT 8
US-09-227-906-8
; Sequence 8, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:

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```

; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-8

```

```

Query Match          75.0%; Score 6; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 DWGRIC 8
        |||||
Db      3 DWGRIC 8

```

RESULT 9

US-08-733-505A-35

```

; Sequence 35, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197

```

```

; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-35

```

```

Query Match          62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 WGRIC 8
        |||||
Db      5 WGRIC 9

```

RESULT 10

US-08-706-741B-70

```

; Sequence 70, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-706-741B-70

Query Match 62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 5 WGRIC 9

RESULT 11

US-08-924-695A-70

; Sequence 70, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-695A-70

Query Match 62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 | | | | |
Db 5 WGRIC 9

RESULT 12

US-08-248-819A-39

; Sequence 39, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:
US-08-248-819A-39

Query Match 62.5%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 |||||
Db 9 WGRIC 13

RESULT 13

US-08-337-646A-57

; Sequence 57, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:

US-08-337-646A-57

Query Match 62.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 9 WGRIC 13

RESULT 14

US-08-927-326-57

; Sequence 57, Application US/08927326

; Patent No. 6184202

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, Stanley J.

; TITLE OF INVENTION: CELL DEATH REGULATORS

; NUMBER OF SEQUENCES: 78

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/927,326

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/337,646

; FILING DATE: 10-NOV-1994

; APPLICATION NUMBER: US 08/248,819

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/112,208

; FILING DATE: 26-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15726A-000620

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

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; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:
US-08-927-326-57
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Query Match          62.5%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Qy      4 WGRIC 8
        |||||
Db      9 WGRIC 13
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RESULT 15

US-08-112-208C-15

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; Sequence 15, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:
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US-08-112-208C-15

Query Match 62.5%; Score 5; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 10 WGRIC 14

Search completed: November 13, 2003, 10:41:56
Job time : 10 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 09:53:11 ; Search time 25.6667 Seconds
(without alignments)
49.473 Million cell updates/sec

Title: US-09-228-866-7
Perfect score: 8
Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 358712

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	8	100.0	8	18	AAW13418		Brain homing pepti
2	8	100.0	8	21	AAB07393		Brain homing pepti
3	8	100.0	8	22	AAE11799		Phage peptide #7 t
4	8	100.0	8	23	AAU10710		Brain homing pepti
5	6	75.0	8	18	AAW13419		Brain homing pepti
6	6	75.0	8	21	AAB07394		Brain homing pepti
7	6	75.0	8	22	AAE11800		Phage peptide #8 t
8	6	75.0	8	23	AAU10711		Brain homing pepti
9	5	62.5	20	22	AAB74174		LMW5-HL BH1 domain
10	5	62.5	21	20	AAW87835		Bcl-2 related prot
11	5	62.5	21	22	AAB74152		LMW5-HL BH1 domain
12	4	50.0	7	20	AAW97429		Shigella-like toxi
13	4	50.0	10	20	AAW95550		Peptide 10 from Bc
14	4	50.0	10	22	AAG97002		Human complementar
15	4	50.0	11	24	ABJ36802		G protein coupled
16	4	50.0	12	22	AAB70476		Bcl-2 protein Bcl-
17	4	50.0	12	22	AAB70478		Bcl-x protein Bcl-
18	4	50.0	13	22	AAB74177		Wild-type BCL2 BH1
19	4	50.0	13	22	AAB74178		BCL2 BH1 domain mu
20	4	50.0	15	19	AAW62156		Agrobacterium faec
21	4	50.0	15	20	AAW87842		Human Bcl-2 domain
22	4	50.0	15	20	AAW87843		Human Bcl-2 domain
23	4	50.0	15	22	AAB74159		Wild-type BCL2 BH1
24	4	50.0	15	22	AAB74160		BCL2 BH1 domain mu
25	4	50.0	15	24	ABP71851		Human EDF-1 protei
26	4	50.0	18	22	ABB45281		Rabbit albumin-bin
27	4	50.0	20	19	AAW56780		Human wild-type BC
28	4	50.0	20	19	AAW56781		Human wild-type BC
29	4	50.0	20	20	AAW87820		Epitope of a Bcl-2
30	4	50.0	20	21	AAB19501		Bcl-2 BH1 domain.
31	4	50.0	20	21	AAB19502		Bcl-XL BH1 domain.
32	4	50.0	20	22	AAB74137		Bax epitope #7. U
33	4	50.0	20	22	AAB74169		BCL2 BH1 domain #2
34	4	50.0	20	22	AAB74171		BCL-XL BH1 domain.
35	4	50.0	21	22	AAB74149		BCL2 BH1 domain #1
36	4	50.0	21	22	AAB74172		MCL-1 BH1 domain.
37	4	50.0	21	22	AAB74173		A1 BH1 domain. Mu
38	3	37.5	7	8	AAP71335		Sequence of cyclo-
39	3	37.5	7	15	AAR45652		Peptide displaying
40	3	37.5	7	16	AAR72585		EMAPII active pept
41	3	37.5	7	16	AAR72586		EMAPII active pept
42	3	37.5	7	16	AAR72587		EMAPII active pept
43	3	37.5	7	17	AAR91830		LDL binding ApoB r
44	3	37.5	7	18	AAW28985		Opioid peptide. S
45	3	37.5	7	18	AAW24346		New peptide which

ALIGNMENTS

RESULT 1

AAW13418

ID AAW13418 standard; Peptide; 8 AA.

XX

AC AAW13418;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;

KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in

PT vivo panning method, specifically to identify brain, kidney,

PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 15; Page 68; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing
 CC peptide that was identified using a novel method for obtaining
 CC molecules that home to a selected organ or tissue. This in vivo
 CC panning method typically involves administering a phage display
 CC library to a subject, and identifying expressed peptides which
 CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
 CC vascular tissue or tumour tissue. The isolated peptides (see
 CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
 CC labels to the selected organ/tissue (claimed) or to identify and/or
 CC isolate target molecules (claimed). The peptides can be directly
 CC identified in vivo, as compared to prior art in vitro screening
 CC methods, which require further examination to see if they maintain
 CC specificity in vivo.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 18; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKDWGRIC 8

Db

|||||||
1 CKDWGRIC 8

RESULT 2

AAB07393

ID AAB07393 standard; peptide; 8 AA.

XX

AC AAB07393;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 7.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..8

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in

PT vivo panning comprises administering a library of diverse peptides

PT linked to a tag which facilitates recovery of these peptides -

XX

PS Example 2; Column 17; 20pp; English.

XX

CC The present sequence is a mouse brain homing peptide. This sequence was
CC identified by using in vivo panning to screen a library of potential
CC organ homing molecules. The present sequence can be used to direct a
CC moiety to a the brain tissue, by linking the moiety to the present
CC sequence. Examples of potential moieties are drugs, toxins or a
CC detectable label. The present sequence contains a DXXR amino acid motif
CC (AAB12027). The DXXR motif resembles the RGD, DGR and NGR motifs that
CC bind to certain integrins.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKDWGRIC 8
 |||||
Db 1 CKDWGRIC 8

RESULT 3

AAE11799

ID AAE11799 standard; peptide; 8 AA.

XX

AC AAE11799;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #7 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo
PT panning that selectively home to a selected organ or tissue useful for
PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 8 AA;

Query Match

100.0%; Score 8; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKDWGRIC 8
 |||||
Db 1 CKDWGRIC 8

RESULT 4

AAU10710

ID AAU10710 standard; peptide; 8 AA.

XX

AC AAU10710;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #7 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;
KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.

XX

PT Recovering molecules that home to an organ or tissue, useful for
PT identifying molecules that home to a specific organ or tissue, e.g.
PT identifying a tumour homing molecule to identify the presence of cancer,
PT by in vivo panning of a library -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering
CC to the subject the library of diverse molecules, collecting a sample of
CC the selected organ or tissue (e.g. brain or kidney), and recovering from
CC the sample several molecules that home to the selected organ or tissue.
CC The method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety
CC (e.g. drug, toxin or detectable label) to the selected organ.
CC Specifically, the method is useful for identifying the presence of cancer

CC in a subject by linking an appropriate moiety to a tumour homing
CC molecule. The present method provides a direct means for identifying
CC molecules that specifically home to a selected organ and, therefore
CC provides a significant advantage over previous methods, which require
CC that a molecule identified using an in vitro screening method
CC subsequently be examined to determine if it maintains its specificity in
CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
CC the present invention.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKDWGRIC 8
|||
Db 1 CKDWGRIC 8

RESULT 5

AAW13419

ID AAW13419 standard; Peptide; 8 AA.

XX

AC AAW13419;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;
KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in
PT vivo panning method, specifically to identify brain, kidney,
PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 15; Page 68; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing

CC peptide that was identified using a novel method for obtaining
CC molecules that home to a selected organ or tissue. This in vivo
CC panning method typically involves administering a phage display
CC library to a subject, and identifying expressed peptides which
CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
CC vascular tissue or tumour tissue. The isolated peptides (see
CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
CC labels to the selected organ/tissue (claimed) or to identify and/or
CC isolate target molecules (claimed). The peptides can be directly
CC identified in vivo, as compared to prior art in vitro screening
CC methods, which require further examination to see if they maintain
CC specificity in vivo.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 18; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 6

AAB07394

ID AAB07394 standard; peptide; 8 AA.

XX

AC AAB07394;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 8.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..8

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in
PT vivo panning comprises administering a library of diverse peptides
PT linked to a tag which facilitates recovery of these peptides -
XX

PS Example 2; Column 17; 20pp; English.
XX

CC The present sequence is a mouse brain homing peptide. This sequence was
CC identified by using in vivo panning to screen a library of potential
CC organ homing molecules. The present sequence can be used to direct a
CC moiety to a the brain tissue, by linking the moiety to the present
CC sequence. Examples of potential moieties are drugs, toxins or a
CC detectable label. The present sequence contains a DXXR amino acid motif
CC (AAB12027). The DXXR motif resembles the RGD, DGR and NGR motifs that
CC bind to certain integrins.
XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWGRIC 8
|||
Db 3 DWGRIC 8

RESULT 7

AAE11800

ID AAE11800 standard; peptide; 8 AA.

XX

AC AAE11800;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #8 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
XX

OS Bacteriophage.

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo
PT panning that selectively home to a selected organ or tissue useful for
PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 2lpp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 8

AAU10711

ID AAU10711 standard; peptide; 8 AA.

XX

AC AAU10711;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #8 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;

KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.
 XX
 PT Recovering molecules that home to an organ or tissue, useful for
 PT identifying molecules that home to a specific organ or tissue, e.g.
 PT identifying a tumour homing molecule to identify the presence of cancer,
 PT by in vivo panning of a library -
 XX
 PS Example 2; Column 17; 21pp; English.
 XX
 CC The present invention relates to a method of recovering molecules that
 CC home to a selected organ or tissue. The method comprises administering
 CC to the subject the library of diverse molecules, collecting a sample of
 CC the selected organ or tissue (e.g. brain or kidney), and recovering from
 CC the sample several molecules that home to the selected organ or tissue.
 CC The method is useful for identifying molecules, particularly useful for
 CC screening large number of molecules (e.g. peptides), that home to a
 CC specific organ. The identified molecule is useful for e.g. raising an
 CC antibody specific for a target molecule, targeting a desired moiety
 CC (e.g. drug, toxin or detectable label) to the selected organ.
 CC Specifically, the method is useful for identifying the presence of cancer
 CC in a subject by linking an appropriate moiety to a tumour homing
 CC molecule. The present method provides a direct means for identifying
 CC molecules that specifically home to a selected organ and, therefore
 CC provides a significant advantage over previous methods, which require
 CC that a molecule identified using an in vitro screening method
 CC subsequently be examined to determine if it maintains its specificity in
 CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
 CC the present invention.
 XX
 SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8
 |||||
 Db 3 DWGRIC 8

RESULT 9
 AAB74174

ID AAB74174 standard; Peptide; 20 AA.
 XX
 AC AAB74174;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE LMW5-HL BH1 domain #2.
 XX
 KW Bax; cytostatic; immunosuppressive; immunostimulant; infection;
 KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
 KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
 KW myocardial infarction; traumatic brain injury; ischaemia; Bcl-2;
 KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
 KW lymphoproliferative disease.
 XX

OS Unidentified.
 XX
 PN US6184202-B1.
 XX
 PD 06-FEB-2001.
 XX
 PF 11-SEP-1997; 97US-0927326.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 2001-256104/26.
 XX
 PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
 PT adult tissues, or treating proliferative or autoimmune diseases,
 PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
 PT bcl-2 associated X protein -
 XX
 PS Example 11; Fig 22; 105pp; English.
 XX
 CC The present invention relates to a method of modulating apoptosis of a
 CC cell. The method comprises administering to the cell an agent,
 CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
 CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
 CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
 CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
 CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
 CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
 CC traumatic brain injury, neurodegenerative diseases, aging, ischaemia,
 CC toxemia, infection, hepatitis, transplant rejection, and
 CC lymphoproliferative diseases. The present sequence is a peptide, which
 CC was used in the method of the present invention.
 XX
 SQ Sequence 20 AA;

 Query Match 62.5%; Score 5; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 WGRIC 8
 |||||
 Db 9 WGRIC 13

RESULT 10
 AAW87835
 ID AAW87835 standard; Peptide; 21 AA.
 XX
 AC AAW87835;
 XX
 DT 10-MAR-1999 (first entry)
 XX

DE Bcl-2 related protein (LMW5-HL) domain BH1 peptide.
 XX
 KW Bcl-2 related protein; Bax; bcl-2; modulator; domain BH1;
 KW bcl-2-related function; apoptosis; dimer; Bcl-xL; Mcl-1; A1.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "Arg or Lys"
 XX
 PN US5856171-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 10-NOV-1994; 94US-0337646.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 1999-105119/09.
 XX
 PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
 PT identifying modulators of bcl-2 function
 XX
 PS Example 10; Fig 14A; 105pp; English.
 XX
 CC AAW87832-36 represent the amino acid sequences of domain BH1 of
 CC Bcl-2-related proteins. The specification describes a composition
 CC comprising a hybrid protein comprising an activator domain of a
 CC transcriptional activator protein and a bcl-2 family member having
 CC a BH1 domain and a BH2 domain; another hybrid protein comprising a
 CC DNA-binding domain of the transcriptional activator protein and a
 CC second bcl-2 family member having a BH1 domain and a BH2 domain; and
 CC a reporter gene linked to a transcriptional regulatory element whose
 CC transcriptional activity is dependent on the presence or absence of
 CC a dimer of the two hybrid proteins. The bcl-2 family members are
 CC selected from naturally occurring Bcl-2, Bcl-xL, Bax, Mcl-1, A1,
 CC fragments thereof, and mutants having a mutation in the BH1 and/or
 CC BH2 domain that alters intermolecular binding of the two bcl-2 family
 CC members. The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2, which
 CC would be potentially useful as drugs for modulating apoptosis.
 XX
 SQ Sequence 21 AA;

 Query Match 62.5%; Score 5; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 |||||

RESULT 11

AAB74152

ID AAB74152 standard; Peptide; 21 AA.

XX

AC AAB74152;

XX

DT 22-MAY-2001 (first entry)

XX

DE LMW5-HL BH1 domain #1.

XX

KW Bax; cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischaemia; Bcl-2;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.

XX

OS Unidentified.

XX

PN US6184202-B1.

XX

PD 06-FEB-2001.

XX

PF 11-SEP-1997; 97US-0927326.

XX

PR 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Korsmeyer SJ;

XX

DR WPI; 2001-256104/26.

XX

PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
PT adult tissues, or treating proliferative or autoimmune diseases,
PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
PT bcl-2 associated X protein -

XX

PS Example 10; Fig 14; 105pp; English.

XX

CC The present invention relates to a method of modulating apoptosis of a
CC cell. The method comprises administering to the cell an agent,
CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
CC traumatic brain injury, neurodegenerative diseases, aging, ischaemia,
CC toxemia, infection, hepatitis, transplant rejection, and
CC lymphoproliferative diseases. The present sequence is a peptide, which
CC was used in the method of the present invention.

XX
SQ Sequence 21 AA;

Query Match 62.5%; Score 5; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||
Db 10 WGRIC 14

RESULT 12

AAW97429

ID AAW97429 standard; peptide; 7 AA.

XX

AC AAW97429;

XX

DT 19-MAY-1999 (first entry)

XX

DE Shigella-like toxin epitope from Escherichia coli O157:H7.

XX

KW Shigella-like toxin; SLT; Escherichia coli O157:H7;
KW epitope; vaccine.

XX

OS Escherichia coli.

XX

PN WO9905169-A1.

XX

PD 04-FEB-1999.

XX

PF 17-JUL-1998; 98WO-GB02156.

XX

PR 21-JUL-1997; 97GB-0015177.

XX

PA (NEUT-) NEUTEC PHARMA PLC.

XX

PI Burnie JP, Matthews RC;

XX

DR WPI; 1999-142851/12.

XX

PT New epitopes of shigella-like toxin (SLT) - useful in the diagnosis
PT and treatment of pathogens expressing SLTs, particularly E. coli
PT O157:H7

XX

PS Claim 1; Page 21; 29pp; English.

XX

CC AAW97424-30 represents epitope of shigella-like toxin (SLT) from
CC Escherichia coli O157:H7. The epitopes and their binding agents
CC are used in the diagnosis and treatment of animals or humans.
CC The epitopes can be used as an immunogen or vaccine.

XX

SQ Sequence 7 AA;

Query Match 50.0%; Score 4; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 1 WGRI 4

RESULT 13

AAW95550

ID AAW95550 standard; peptide; 10 AA.

XX

AC AAW95550;

XX

DT 26-MAR-1999 (first entry)

XX

DE Peptide 10 from Bcl-2-related family.

XX

KW Cytochrome C; apoptotic; Bcl-2; neurodegeneration; Bcl-xL; cancer;
KW autoimmune disease; rheumatoid arthritis; transplant rejection; AIDS;
KW insulin-dependent diabetes mellitus.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9858541-A1.

XX

PD 30-DEC-1998.

XX

PF 16-JUN-1998; 98WO-US12595.

XX

PR 24-JUN-1997; 97US-0881646.

XX

PA (DAND) DANA FARBER CANCER INST INC.

PA (NOVS) NOVARTIS AG.

XX

PI Kharbanda SM, Kufe DW, Nalin CM, Sharma SK;

XX

DR WPI; 1999-080967/07.

XX

PT New peptides that inhibit binding of cytochrome C to anti-apoptotic
PT Bcl-2 proteins - useful in the treatment of autoimmune disease,
PT transplant rejection and cancer, and also in screening for
PT modulators of apoptosis

XX

PS Example 3; Page 14; 64pp; English.

XX

CC The invention relates to a peptide that inhibits binding of cytochrome C
CC to an anti-apoptotic member of the Bcl-2 family. The peptides are used
CC to screen for compounds that promote or inhibit apoptosis (for treating
CC neurodegeneration). The peptides, or peptidomimetics, are used to
CC inhibit binding of cytochrome C to Bcl-xL in mammalian cells. This is
CC used to treat autoimmune diseases (e.g. rheumatoid arthritis or
CC insulin-dependent diabetes mellitus), transplant rejection and cancer,
CC optionally in combination with chemotherapy, radiotherapy or
CC immunotherapy. Nucleic acid encoding polypeptides that include the
CC peptide (AAW95539-42) sequences is used to inhibit release of cytochrome
CC C into the cytosol, specifically in patients with acquired immune
CC deficiency syndrome, and also to promote survival of haematopoietic cells

CC in patients undergoing chemo- or radio- therapy. Antibodies that bind
CC specifically to an epitope in peptides AAW95539-42 are used to determine
CC Bcl-xL or Bcl-2, for diagnosis or prognosis, and also in screening
CC assays. Administration of the peptides in targeting vehicles may
CC eliminate specific pathogenic cells without harming the rest of the
CC immune system. Sequences AAW95543-52 represents peptide fragments from
CC Bcl-2-related family that were used in assays for inhibition of binding
CC of fused GST-Bcl-xL to cytochrome C

XX

SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7

||||

Db 4 WGRI 7

RESULT 14

AAG97002

ID AAG97002 standard; Peptide; 10 AA.

XX

AC AAG97002;

XX

DT 18-SEP-2001 (first entry)

XX

DE Human complementary peptide, SEQ ID NO: 3196.

XX

KW Human; complementary peptide; ligand; drug discovery; drug design.

XX

OS Homo sapiens.

XX

PN WO200142277-A2.

XX

PD 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-GB04776.

XX

PR 13-DEC-1999; 99GB-0029464.

XX

PA (PROT-) PROTEOM LTD.

XX

PI Roberts GW, Heal JR;

XX

DR WPI; 2001-408419/43.

XX

PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -

XX

PS Example 4; Page 503; 646pp; English.

XX

CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides

CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.

XX

SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8

||||

Db 7 GRIC 10

RESULT 15

ABJ36802

ID ABJ36802 standard; Peptide; 11 AA.

XX

AC ABJ36802;

XX

DT 01-MAY-2003 (first entry)

XX

DE G protein coupled receptor related peptide SEQ ID No 149.

XX

KW Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
KW antibacterial; analgesic; antiallergic; antiasthmatic; antiinflammatory;
KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;
KW G protein coupled receptor signaling inhibitor; GPCR; library;
KW high throughput screening assay; stroke; myocardial infarction;
KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
KW septic shock; pain; allergic disorder; inflammatory bowel disease;
KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
KW schizophrenia; Alzheimer's disease.

XX

OS Unidentified.

XX

PN WO200272778-A2.

XX

PD 19-SEP-2002.

XX

PF 14-MAR-2002; 2002WO-US07561.

XX

PR 14-MAR-2001; 2001US-275472P.

PR 11-MAY-2001; 2001US-0852910.

XX

PA (CUEB-) CUE BIOTECH.

XX

PI Gilchrist A, Hamm HE;

XX

DR WPI; 2003-247841/24.

XX

PT Identifying G protein coupled receptor (GPCR) signaling inhibitors,
PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signaling with high
PT affinity and specificity -

XX

PS Claim 94; Page 63; 94pp; English.

XX

CC The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signaling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signaling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention.

XX

SQ Sequence 11 AA;

Query Match 50.0%; Score 4; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KDWG 5

||||

Db 6 KDWG 9

Search completed: November 13, 2003, 10:32:55

Job time : 25.6667 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:38:27 ; Search time 15.6667 Seconds
(without alignments)
93.222 Million cell updates/sec

Title: US-09-228-866-7

Perfect score: 8

Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 124183

Minimum DB seq length: 7

Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	62.5	21	15	US-10-277-693A-15	Sequence 15, Appl
2	4	50.0	8	15	US-10-101-482-1	Sequence 1, Appli
3	4	50.0	10	11	US-09-572-404B-3196	Sequence 3196, App
4	4	50.0	11	11	US-09-852-910-149	Sequence 149, App
5	4	50.0	15	15	US-10-277-693A-22	Sequence 22, Appl
6	4	50.0	15	15	US-10-277-693A-23	Sequence 23, Appl
7	4	50.0	17	12	US-10-280-066-83	Sequence 83, Appl
8	4	50.0	18	11	US-09-539-443-52	Sequence 52, Appl
9	4	50.0	21	15	US-10-277-693A-12	Sequence 12, Appl
10	3	37.5	7	10	US-09-851-026-3	Sequence 3, Appli
11	3	37.5	7	10	US-09-851-026-9	Sequence 9, Appli
12	3	37.5	7	10	US-09-851-026-10	Sequence 10, Appl
13	3	37.5	7	10	US-09-851-026-37	Sequence 37, Appl
14	3	37.5	7	10	US-09-813-718-26	Sequence 26, Appl
15	3	37.5	7	10	US-09-813-718-27	Sequence 27, Appl
16	3	37.5	7	10	US-09-813-718-31	Sequence 31, Appl
17	3	37.5	7	10	US-09-813-718-33	Sequence 33, Appl
18	3	37.5	7	10	US-09-884-767A-63	Sequence 63, Appl
19	3	37.5	7	12	US-10-190-082-44	Sequence 44, Appl
20	3	37.5	7	12	US-10-300-699-46	Sequence 46, Appl

21	3	37.5	7	12	US-10-257-050-12	Sequence 12, Appl
22	3	37.5	7	12	US-10-319-402-8	Sequence 8, Appli
23	3	37.5	7	12	US-10-319-402-10	Sequence 10, Appl
24	3	37.5	8	11	US-09-880-748-2982	Sequence 2982, Ap
25	3	37.5	8	11	US-09-972-656-62	Sequence 62, Appl
26	3	37.5	8	12	US-09-932-165-1442	Sequence 1442, Ap
27	3	37.5	8	12	US-10-348-504-70	Sequence 70, Appl
28	3	37.5	8	12	US-10-348-504-71	Sequence 71, Appl
29	3	37.5	8	12	US-10-348-504-72	Sequence 72, Appl
30	3	37.5	8	12	US-10-348-504-73	Sequence 73, Appl
31	3	37.5	8	12	US-10-348-504-74	Sequence 74, Appl
32	3	37.5	8	12	US-10-348-504-109	Sequence 109, App
33	3	37.5	8	12	US-10-348-504-118	Sequence 118, App
34	3	37.5	8	12	US-09-848-107-16	Sequence 16, Appl
35	3	37.5	8	12	US-10-319-402-9	Sequence 9, Appli
36	3	37.5	8	12	US-10-319-402-31	Sequence 31, Appl
37	3	37.5	8	12	US-10-407-123-44	Sequence 44, Appl
38	3	37.5	8	12	US-10-407-123-45	Sequence 45, Appl
39	3	37.5	8	12	US-10-407-123-46	Sequence 46, Appl
40	3	37.5	8	12	US-10-407-123-47	Sequence 47, Appl
41	3	37.5	8	12	US-10-407-123-49	Sequence 49, Appl
42	3	37.5	8	12	US-10-407-123-84	Sequence 84, Appl
43	3	37.5	8	12	US-10-407-123-94	Sequence 94, Appl
44	3	37.5	8	14	US-10-095-450-35	Sequence 35, Appl
45	3	37.5	9	8	US-08-424-550B-357	Sequence 357, App

ALIGNMENTS

RESULT 1
 US-10-277-693A-15
 ; Sequence 15, Application US/10277693A
 ; Publication No. US20030096367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korsmeyer, Stanley J.
 ; TITLE OF INVENTION: Cell Death Agonists
 ; FILE REFERENCE: 56029/36280
 ; CURRENT APPLICATION NUMBER: US/10/277,693A
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: 09/379,820
 ; PRIOR FILING DATE: 1999-08-24
 ; PRIOR APPLICATION NUMBER: 08/112,208
 ; PRIOR FILING DATE: 1993-08-26
 ; PRIOR APPLICATION NUMBER: 08/856,034
 ; PRIOR FILING DATE: 1997-05-14
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; FEATURE:
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION:
 ; FEATURE:

; NAME/KEY: MISC_FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Amino acid is either K (Lys) or R (Arg)
US-10-277-693A-15

Query Match 62.5%; Score 5; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
||||
Db 10 WGRIC 14

RESULT 2

US-10-101-482-1

; Sequence 1, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-101-482-1

Query Match 50.0%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGR 6
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Db 1 DWGR 4

RESULT 3

US-09-572-404B-3196
; Sequence 3196, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3196
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERBB3 OR HER3 at 523-532 and may
interact with
; OTHER INFORMATION: Sequence 3195 in this patent.
US-09-572-404B-3196

Query Match 50.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8
|||
Db 7 GRIC 10

RESULT 4

US-09-852-910-149
; Sequence 149, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled
Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G alpha t library sequence
US-09-852-910-149

Query Match 50.0%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KDWG 5
|||
Db 6 KDWG 9

RESULT 5

US-10-277-693A-22
; Sequence 22, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Murine
US-10-277-693A-22

Query Match 50.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 10 WGRI 13

RESULT 6

US-10-277-693A-23
; Sequence 23, Application US/10277693A

; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Murine
US-10-277-693A-23

Query Match 50.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 10 WGRI 13

RESULT 7
US-10-280-066-83
; Sequence 83, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING
TARGET BINDERS
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC_FEATURE

; OTHER INFORMATION: DGI-2-20R-4-G22
US-10-280-066-83

Query Match 50.0%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGR 6
|||
Db 6 DWGR 9

RESULT 8

US-09-539-443-52

; Sequence 52, Application US/09539443
; Publication No. US20030100483A1

; GENERAL INFORMATION:

; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-539-443-52

Query Match 50.0%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8
|||
Db 3 GRIC 6

RESULT 9

US-10-277-693A-12
; Sequence 12, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Murine
US-10-277-693A-12

Query Match 50.0%; Score 4; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 11 WGRI 14

RESULT 10

US-09-851-026-3
; Sequence 3, Application US/09851026
; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host
Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:

```

;      ADDRESSEE: Cooper & Dunham, LLP
;      STREET: 1185 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: USA
;      ZIP: 10036
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.30, Version #1.30
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/851,026
;      FILING DATE: 07-May-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/360,821
;      FILING DATE: 08-OCT-96
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: White, John P.
;      REGISTRATION NUMBER: 28,678
;      REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 212-278-0400
;      TELEFAX: 212-391-0525
;
;      INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 7 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: Peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-851-026-3

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Query Match          37.5%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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QY      5 GRI 7
      |||
Db      3 GRI 5

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RESULT 11

US-09-851-026-9

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; Sequence 9, Application US/09851026
; Patent No. US20020160957A1

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GENERAL INFORMATION:

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;      APPLICANT: Stern, David M.
;      Clauss, Matthias
;      Kao, Janet
;      Kayton, Mark
;      Libutti, Steven K

```

```

;      TITLE OF INVENTION: Endothelial Monocyte Activating
;                          Polypeptide II: A Mediator Which Activates Host
Response

```



```

;      NUMBER OF SEQUENCES: 42
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Cooper & Dunham, LLP
;          STREET: 1185 Avenue of the Americas
;          CITY: New York
;          STATE: New York
;          COUNTRY: USA
;          ZIP: 10036
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.30, Version #1.30
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/851,026
;          FILING DATE: 07-May-2001
;          CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/360,821
;          FILING DATE: 08-OCT-96
;      ATTORNEY/AGENT INFORMATION:
;          NAME: White, John P.
;          REGISTRATION NUMBER: 28,678
;          REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 212-278-0400
;          TELEFAX: 212-391-0525
;      INFORMATION FOR SEQ ID NO: 9:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 7 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: Peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-851-026-9

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Query Match          37.5%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      5 GRI 7
      |||
Db      3 GRI 5

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RESULT 12
US-09-851-026-10
; Sequence 10, Application US/09851026
; Patent No. US20020160957A1
;   GENERAL INFORMATION:
;       APPLICANT: Stern, David M.
;               Clauss, Matthias
;               Kao, Janet
;               Kayton, Mark
;               Libutti, Steven K
;   TITLE OF INVENTION: Endothelial Monocyte Activating

```

```

;                                     Polypeptide II:  A Mediator Which Activates Host
Response
;      NUMBER OF SEQUENCES: 42
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Cooper & Dunham, LLP
;          STREET: 1185 Avenue of the Americas
;          CITY: New York
;          STATE: New York
;          COUNTRY: USA
;          ZIP: 10036
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.30, Version #1.30
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/851,026
;          FILING DATE: 07-May-2001
;          CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/360,821
;          FILING DATE: 08-OCT-96
;      ATTORNEY/AGENT INFORMATION:
;          NAME: White, John P.
;          REGISTRATION NUMBER: 28,678
;          REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 212-278-0400
;          TELEFAX: 212-391-0525
;      INFORMATION FOR SEQ ID NO: 10:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 7 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: Peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-851-026-10

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Query Match          37.5%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      5 GRI 7
        |||
Db      3 GRI 5

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RESULT 13
US-09-851-026-37
; Sequence 37, Application US/09851026
; Patent No. US20020160957A1
;   GENERAL INFORMATION:
;       APPLICANT: Stern, David M.
;               Clauss, Matthias
;               Kao, Janet
;               Kayton, Mark

```

```

;           Libutti, Steven K
;   TITLE OF INVENTION: Endothelial Monocyte Activating
;                       Polypeptide II: A Mediator Which Activates Host
Response
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Cooper & Dunham, LLP
;       STREET: 1185 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10036
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.30, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/851,026
;       FILING DATE: 07-May-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/360,821
;       FILING DATE: 08-OCT-96
;   ATTORNEY/AGENT INFORMATION:
;       NAME: White, John P.
;       REGISTRATION NUMBER: 28,678
;       REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 212-278-0400
;       TELEFAX: 212-391-0525
;   INFORMATION FOR SEQ ID NO: 37:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 7 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-851-026-37

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```

Query Match          37.5%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      5 GRI 7
        |||
Db      2 GRI 4

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```

RESULT 14
US-09-813-718-26
; Sequence 26, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke

```

; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-718-26

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 3 GRI 5

RESULT 15

US-09-813-718-27

; Sequence 27, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-813-718-27

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 3 GRI 5

Search completed: November 13, 2003, 11:12:33
Job time : 16.6667 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:26:01 ; Search time 7.83333 Seconds
(without alignments)
98.215 Million cell updates/sec

Title: US-09-228-866-7
Perfect score: 8
Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3752

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	37.5	7	2	PT0628	T-cell receptor be	
2	3	37.5	7	2	PT0642	T-cell receptor be	
3	3	37.5	7	2	PT0722	T-cell receptor be	
4	3	37.5	7	2	PT0728	T-cell receptor be	
5	3	37.5	8	2	PT0724	T-cell receptor be	
6	3	37.5	10	2	A40753	aldehyde ferredoxi	
7	3	37.5	10	2	PH1344	Ig heavy chain DJ	
8	3	37.5	10	2	PH0923	T-cell receptor be	
9	3	37.5	12	2	I46922	gene Bota protein	
10	3	37.5	13	2	PH0928	T-cell receptor be	
11	3	37.5	15	2	I46512	troponin - rabbit	
12	3	37.5	15	2	JT0610	leukocyte chemoatt	
13	3	37.5	17	2	I46511	troponin - rabbit	
14	3	37.5	17	2	I67526	CD33 antigen homol	
15	3	37.5	18	2	S49026	ribosomal protein	
16	3	37.5	19	2	PS0236	trypsin inhibitor	
17	3	37.5	19	2	A28814	Ig kappa chain V r	

18	3	37.5	19	2	S12268	Qa-2 antigen - mou
19	3	37.5	19	2	I49037	TcR delta chain V-
20	3	37.5	20	2	S65399	immunodeficiency v
21	3	37.5	20	2	PC4384	DnaK protein homol
22	3	37.5	20	2	S28435	major outer membra
23	3	37.5	20	2	PQ0071	T-cell receptor be
24	3	37.5	21	2	B12055	glyceraldehyde-3-p
25	2	25.0	7	2	S16364	opacity protein P.
26	2	25.0	7	2	S16365	opacity protein P.
27	2	25.0	7	2	S57274	triacylglycerol li
28	2	25.0	7	2	PT0526	T-cell receptor be
29	2	25.0	7	2	PT0667	T-cell receptor be
30	2	25.0	7	2	PT0655	T-cell receptor be
31	2	25.0	7	2	PT0688	T-cell receptor be
32	2	25.0	7	2	PT0586	T-cell receptor be
33	2	25.0	7	2	B48394	major fat-globule
34	2	25.0	7	2	PD0029	pev-kinin 1 - pena
35	2	25.0	8	2	S15422	adipokinetic hormo
36	2	25.0	8	2	S11545	adipokinetic hormo
37	2	25.0	8	2	A58641	adipokinetic hormo
38	2	25.0	8	2	S59622	metallothionein is
39	2	25.0	8	2	A31570	angiotensin-conver
40	2	25.0	8	2	S70727	ipgF protein - Shi
41	2	25.0	8	2	C61512	variant surface gl
42	2	25.0	8	2	D61512	variant surface gl
43	2	25.0	8	2	JS0315	leucokinin V - Mad
44	2	25.0	8	2	JS0316	leucokinin VI - Ma
45	2	25.0	8	2	JS0317	leucokinin VII - M

ALIGNMENTS

RESULT 1

PT0628

T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0628

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0628

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5

|||

Db

5 DWG 7

RESULT 2

PT0642

T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0642

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0642

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5

|||

Db 4 DWG 6

RESULT 3

PT0722

T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0722

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0722

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5

|||

Db 5 DWG 7

RESULT 4

PT0728

T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0728

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0728

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWG 5
|||
Db 4 DWG 6

RESULT 5

PT0724

T-cell receptor beta chain V-D-J region (140-2C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0724; PT0555

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0724

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-8 <FEE>

A;Experimental source: newborn thymus, strain BALB/c (clone 140-2C)

A;Accession: PT0555

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <FE2>

A;Experimental source: day 18 fetal thymus, strain BALB/c (clone 126-1AL)

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWG 5
|||
Db 6 DWG 8

RESULT 6

A40753

aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) - Pyrococcus furiosus (fragment)
N;Alternate names: glyceraldehyde:ferredoxin oxidoreductase; red tungsten
protein (RTP)

C;Species: Pyrococcus furiosus

C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1996

C;Accession: A40753

R;Mukund, S.; Adams, M.W.W.

J. Biol. Chem. 266, 14208-14216, 1991

A;Title: The novel tungsten-iron-sulfur protein of the hyperthermophilic
archaebacterium, Pyrococcus furiosus, is an aldehyde ferredoxin oxidoreductase.
Evidence for its participation in a unique glycolytic pathway.

A;Reference number: A40753; MUID:91317766; PMID:1907273

A;Accession: A40753

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <MUK>

C;Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGR 6

|||

Db 5 WGR 7

RESULT 7

PH1344

Ig heavy chain DJ region (clone C100-91A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1344

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B
precursor lymphoblastic leukemia as evidence for an in utero transforming event.

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1344

A;Molecule type: DNA

A;Residues: 1-10 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5

|||

Db 5 DWG 7

RESULT 8

PH0923

T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0923
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0923
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGR 6
|||
Db 4 WGR 6

RESULT 9

I46922

gene Bota protein - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46922
R;Ellis, S.A.; Braem, K.A.; Morrison, W.I.
Immunogenetics 37, 49-56, 1992
A;Title: Transmembrane and cytoplasmic domain sequences demonstrate at least two
expressed bovine MHC class I loci.
A;Reference number: I46921; MUID:93052564; PMID:1428011
A;Accession: I46922
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-12 <ELL>
A;Cross-references: GB:S47738; NID:g258999; PIDN:AAB23972.1; PID:g259000
C;Genetics:
A;Gene: Bota

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 4 GRI 6

RESULT 10

PH0928

T-cell receptor beta chain V-D-J region (clone 14) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0928
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
 allergic encephalomyelitis: conserved complementarity determining region 3.
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0928
 A;Molecule type: mRNA
 A;Residues: 1-13 <GOL>
 A;Experimental source: concanavalin A-activated lymphoblast
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
 |||
 Db 7 DWG 9

RESULT 11

I46512
 troponin - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
 C;Accession: I46512
 R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
 Nature 302, 718-721, 1983
 A;Title: A new troponin T and cDNA clones for 13 different muscle proteins,
 found by shotgun sequencing.
 A;Reference number: I46471; MUID:83167564; PMID:6687628
 A;Accession: I46512
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-15 <PUT>
 A;Cross-references: EMBL:V00896; NID:g1734; PIDN:CAA24261.1; PID:g929766
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: EF hand

Query Match 37.5%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 13 GRI 15

RESULT 12

JT0610
 leukocyte chemoattractant peptide 9 - sheep
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Jan-2001
 C;Accession: JT0610
 R;Murdoch, W.J.; McCormick, R.J.

Biochem. Biophys. Res. Commun. 184, 848-852, 1992
A;Title: Sequence analysis of leukocyte chemoattractant peptides secreted by periovulatory ovine follicles.
A;Reference number: JT0609; MUID:92246975; PMID:1575752
A;Accession: JT0610
A;Molecule type: protein
A;Residues: 1-15 <MUR>
C;Superfamily: unassigned animal peptides

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 9 GRI 11

RESULT 13

I46511
troponin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C;Accession: I46511
R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A;Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shotgun sequencing.
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-17 <PUT>
A;Cross-references: EMBL:V00895; NID:g1732; PIDN:CAA24260.1; PID:g929765
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand

Query Match 37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 13 GRI 15

RESULT 14

I67526
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
C;Accession: I67526
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is not accompanied by somatic mutation of VH genes.
A;Reference number: I53392; MUID:94298870; PMID:8026526

A;Accession: I67526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-17 <RES>
A;Cross-references: GB:S71350; NID:g550038
C;Genetics:
A;Gene: VH7183

Query Match 37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 12 DWG 14

RESULT 15

S49026

ribosomal protein HS25 [validated] - Haloarcula marismortui (fragment)

C;Species: Haloarcula marismortui

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C;Accession: S49026; S63967

R;Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.

submitted to the Protein Sequence Database, November 1994

A;Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloarcula marismortui.

A;Reference number: S49023

A;Accession: S49026

A;Molecule type: protein

A;Residues: 1-18 <ENG>

R;Engemann, S.; Noelle, R.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.

Eur. J. Biochem. 234, 24-31, 1995

A;Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloarcula marismortui and complete sequence analysis of protein HS26.

A;Reference number: S63964; MUID:96096717; PMID:8529646

A;Accession: S63967

A;Molecule type: protein

A;Residues: 1-18 <ENW>

C;Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match 37.5%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 5 GRI 7

Search completed: November 13, 2003, 10:39:55
Job time : 7.83333 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 09:55:06 ; Search time 4.33333 Seconds
(without alignments)
86.819 Million cell updates/sec

Title: US-09-228-866-7
Perfect score: 8
Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1246

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3	37.5	13	1	TEML_RANTE	P57104 rana tempor
2	3	37.5	15	1	ITRB_ALBJU	P24927 albizzia ju
3	3	37.5	20	1	CUDP_VERCH	P80406 verticilliu
4	3	37.5	21	1	ATPB_PHYPA	P80658 physcomitre
5	3	37.5	21	1	SRTD_ATREN	P13211 atractaspis
6	2	25.0	8	1	ACI_THUAL	P18691 thunnus alb
7	2	25.0	8	1	AKH_MELML	P25423 melolontha
8	2	25.0	8	1	LCK1_LEUMA	P21140 leucophaea
9	2	25.0	8	1	LCK2_LEUMA	P21141 leucophaea
10	2	25.0	8	1	LCK3_LEUMA	P21142 leucophaea
11	2	25.0	8	1	LCK4_LEUMA	P21143 leucophaea
12	2	25.0	8	1	LCK5_LEUMA	P19987 leucophaea
13	2	25.0	8	1	LCK6_LEUMA	P19988 leucophaea
14	2	25.0	8	1	LCK7_LEUMA	P19989 leucophaea
15	2	25.0	8	1	LCK8_LEUMA	P19990 leucophaea
16	2	25.0	8	1	RT34_BOVIN	P82929 bos taurus
17	2	25.0	9	1	FAR6_MACRS	P83279 macrobrachi
18	2	25.0	9	1	FIBB_ERYPA	P19346 erythrocebu
19	2	25.0	9	1	FIBB_MACFU	P19345 macaca fusc

20	2	25.0	9	1	FIBB_PAPAN	P19344	papio anubi
21	2	25.0	9	1	FIBB_PAPHA	P19343	papio hamad
22	2	25.0	9	1	FIBB_THEGE	P19342	theropithec
23	2	25.0	9	1	IPYR_RHOVI	P82992	rhodopseudo
24	2	25.0	9	1	PGLR_DIAAB	P81179	diaprepes a
25	2	25.0	9	1	RS10_SERMA	O68936	serratia ma
26	2	25.0	10	1	AKHX_LOCFI	P81626	locusta mig
27	2	25.0	10	1	BPP8_BOTIN	P30426	bothrops in
28	2	25.0	10	1	GON3_PETMA	P30948	petromyzon
29	2	25.0	10	1	HTF1_ROMMI	P18110	romalea mic
30	2	25.0	10	1	HTF2_CARMO	P11385	carausius m
31	2	25.0	10	1	HTF_HELZE	P16353	heliothis z
32	2	25.0	10	1	HTF_NAUCI	P10939	nauphoeta c
33	2	25.0	10	1	HTF_TABAT	P14596	tabanus atr
34	2	25.0	10	1	LABA_JATMU	P13270	jatropha mu
35	2	25.0	10	1	MALE_KLEPN	Q05564	klebsiella
36	2	25.0	10	1	SP34_DICMU	P81545	dictyosteli
37	2	25.0	10	1	SPI_HALRO	Q10997	halocynthia
38	2	25.0	10	1	TPIS_NICPL	P19118	nicotiana p
39	2	25.0	10	1	UPA5_HUMAN	P30091	homo sapien
40	2	25.0	10	1	UXA6_CHLTR	P38007	chlamydia t
41	2	25.0	10	1	XYNB_DICB4	P80717	dictyoglomu
42	2	25.0	11	1	ANGT_CRIGE	P09037	crinia geor
43	2	25.0	11	1	BPP_AGKHP	P04562	agkistrodon
44	2	25.0	11	1	CEP1_ACHFU	P22790	achatina fu
45	2	25.0	11	1	FAR6_PENMO	P83321	penaeus mon

ALIGNMENTS

RESULT 1

TEML_RANTE

ID TEML_RANTE STANDARD; PRT; 13 AA.

AC P57104;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Temporin L.

OS Rana temporaria (European common frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8407;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=97175050; PubMed=9022710;

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

RA Barra D.;

RT "Temporins, antimicrobial peptides from the European red frog Rana

RT temporaria.";

RL Eur. J. Biochem. 242:788-792(1996).

CC !- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND

CC GRAM-POSITIVE BACTERIA.

CC !- SUBCELLULAR LOCATION: Secreted.

CC !- TISSUE SPECIFICITY: Skin.

CC !- SIMILARITY: Belongs to the brevinin family.

KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 10 GRI 12

RESULT 2

ITRB_ALBJU

ID ITRB_ALBJU STANDARD; PRT; 15 AA.
AC P24927;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin inhibitor B chain (Fragment).
OS Albizzia julibrissin (Silk tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizia.
OX NCBI_TaxID=3813;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=80115605; PubMed=528539;
RA Odani S., Ono T., Ikenaka T.;
RT "Proteinase inhibitors from a mimosoideae legume, Albizzia
RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL J. Biochem. 86:1795-1805(1979).
CC -!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
CC -!- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
CC FAMILY.
KW Serine protease inhibitor.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKD 3
|||
Db 5 CKD 7

RESULT 3

CUDP_VERCH

ID CUDP_VERCH STANDARD; PRT; 20 AA.
AC P80406;
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cuticle-degrading protease-like protein (EC 3.4.21.-) (Chymoelastase)
 DE (Fragment).
 OS *Verticillium chlamydosporium*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Verticillium*.
 OX NCBI_TaxID=40265;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VC10;
 RX MEDLINE=95247009; PubMed=7729666;
 RA Segers R., Butt T.M., Keen J.N., Kerry B.R., Peberdy J.F.;
 RT "The subtilisins of the invertebrate mycopathogens *Verticillium*
 RT *chlamydosporium* and *Metarhizium anisopliae* are serologically and
 RT functionally related."
 RL FEMS Microbiol. Lett. 126:227-231(1995).
 CC -!- FUNCTION: CAPABLE OF BREACHING THE INSECT CUTICLE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to peptidase family S8.
 DR MEROPS; S08.056; -.
 DR InterPro; IPR000209; Peptidase_S8.
 DR PROSITE; PS00136; SUBTILASE_ASP; PARTIAL.
 DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
 DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
 KW Hydrolase; Serine protease.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2113 MW; 26744EC2F7729B19 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 13 GRI 15

RESULT 4

ATPB_PHYPA

ID ATPB_PHYPA STANDARD; PRT; 21 AA.
 AC P80658;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP synthase beta chain (EC 3.6.3.14) (Fragment).
 GN ATPB.
 OS *Physcomitrella patens* (Moss).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Funariidae; Funariales; Funariaceae; *Physcomitrella*.
 OX NCBI_TaxID=3218;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE=97275459; PubMed=9129336;
 RA Kasten B., Buck F., Nuske J., Reski R.;

RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; Chloroplast; Thylakoid; Membrane; CF(1);
KW Hydrolase; ATP-binding; Hydrogen ion transport.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2298 MW; 9558E4F5AC89D81A CRC64;

Query Match 37.5%; Score 3; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 5

SRTD_ATREN
ID SRTD_ATREN STANDARD; PRT; 21 AA.
AC P13211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sarafotoxin-D (S6D) (SRTX-D).
OS Atractaspis engaddensis (Israeli burrowing asp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Atractaspididae; Atractaspis.
OX NCBI_TaxID=8600;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90033283; PubMed=2509240;
RA Bdolah A., Wollberg Z., Fleminger G.;
RT "SRTX-d, a new native peptide of the endothelin/sarafotoxin family.";
RL FEBS Lett. 256:1-3(1989).
CC -!- FUNCTION: VASOCONSTRICTOR ACTIVITY. THESE TOXINS CAUSE CARDIAC
CC ARREST PROBABLY AS A RESULT OF CORONARY VASOSPASM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: LD(50) IS 0.35 MG/KG BY INTRAVENOUS INJECTION.
CC -!- SIMILARITY: BELONGS TO THE ENDOTHELIN/SARAFOTOXIN FAMILY.
DR HSSP; P13208; 1SRB.
DR InterPro; IPR001928; Endothln_tox.

DR InterPro; IPR003642; Sara/bib_toxin.
 DR Pfam; PF00322; endothelin; 1.
 DR ProDom; PD004740; Sara/bib_toxin; 1.
 DR SMART; SM00272; END; 1.
 DR PROSITE; PS00270; ENDOTHELIN; 1.
 KW Vasoconstrictor; Toxin.
 FT DISULFID 1 15 BY SIMILARITY.
 FT DISULFID 3 11 BY SIMILARITY.
 SQ SEQUENCE 21 AA; 2596 MW; 83A8A04D1D536AE2 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKD 3
 |||
 Db 3 CKD 5

RESULT 6

ACI_THUAL

ID ACI_THUAL STANDARD; PRT; 8 AA.
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
 RT muscle.";
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR; A31570; A31570.
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
 ||
 Db 6 WG 7

RESULT 7

AKH_MELML

ID AKH_MELML STANDARD; PRT; 8 AA.
 AC P25423;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Melolontha melolontha (Cockchafer),
 OS Geotrupes stercorosus (Dor beetle), and
 OS Pachnoda marginata (Flower beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
 OC Scarabaeidae; Melolonthinae; Melolontha.
 OX NCBI_TaxID=7061, 7087, 7058;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=91248100; PubMed=2039445;
 RA Gaede G.;
 RT "A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RT sequenced from two beetle species.";
 RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetonid beetle species determined by
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A58641; A58641.
 DR PIR; S15422; S15422.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DW 4
 ||
 Db 7 DW 8

RESULT 8
 LCK1_LEUMA
 ID LCK1_LEUMA STANDARD; PRT; 8 AA.
 AC P21140;

DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin I (L-I).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:205-211(1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
 ||
 Db 7 WG 8

RESULT 9

LCK2_LEUMA

ID LCK2_LEUMA STANDARD; PRT; 8 AA.
 AC P21141;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin II (L-II).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:205-211(1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
||
Db 7 WG 8

RESULT 10

LCK3_LEUMA

ID LCK3_LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
||
Db 7 WG 8

RESULT 11

LCK4_LEUMA

ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)

DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins."
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
 ||
 Db 7 WG 8

RESULT 12

LCK5_LEUMA

ID LCK5_LEUMA STANDARD; PRT; 8 AA.
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=28777794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
 RT myotropic peptides of Leucophaea maderae."
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR; JS0315; JS0315.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
||
Db 7 WG 8

RESULT 13

LCK6_LEUMA

ID LCK6_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
||
Db 7 WG 8

RESULT 14

LCK7_LEUMA

ID LCK7_LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinins VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR; JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDC76A CRC64;

 Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
 ||
 Db 7 WG 8

RESULT 15

LCK8_LEUMA

ID LCK8_LEUMA STANDARD; PRT; 8 AA.
 AC P19990;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinins VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR; JS0318; JS0318.

KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
||
Db 7 WG 8

Search completed: November 13, 2003, 10:33:59
Job time : 4.33333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:58:36 ; Search time 19.6667 Seconds
(without alignments)
104.971 Million cell updates/sec

Title: US-09-228-866-7
Perfect score: 8
Sequence: 1 CKDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7516

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*

```

13:  sp_vertebrate:*
14:  sp_unclassified:*
15:  sp_rvirus:*
16:  sp_bacteriap:*
17:  sp_archeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	4	50.0	17	2	O06946	O06946 salmonella
2	3	37.5	8	2	O32560	O32560 escherichia
3	3	37.5	9	8	Q8MBF4	Q8mbf4 ipomoea qua
4	3	37.5	10	8	Q8MAZ9	Q8maz9 dicranostyl
5	3	37.5	10	8	Q8MBB7	Q8mbb7 merremia ae
6	3	37.5	11	8	Q8MAZ1	Q8maz1 maripa pani
7	3	37.5	11	8	Q8MB39	Q8mb39 wilsonia hu
8	3	37.5	11	8	Q8MB58	Q8mb58 seddera hir
9	3	37.5	11	8	Q8MAZ3	Q8maz3 maripa repe
10	3	37.5	11	8	Q8MBE1	Q8mbel ipomoea alb
11	3	37.5	11	8	Q8MB77	Q8mb77 odonellia h
12	3	37.5	11	8	Q8MB79	Q8mb79 aniseia arg
13	3	37.5	11	8	Q8MB97	Q8mb97 merremia pe
14	3	37.5	12	7	Q31006	Q31006 bos taurus
15	3	37.5	12	8	Q8MAX7	Q8max7 tridynamia
16	3	37.5	14	2	Q93CI1	Q93ci1 escherichia
17	3	37.5	14	4	Q9UHM5	Q9uhm5 homo sapien
18	3	37.5	14	10	P82327	P82327 pisum sativ
19	3	37.5	15	2	Q47892	Q47892 fremyella d
20	3	37.5	15	4	Q9BQT3	Q9bqt3 homo sapien
21	3	37.5	15	11	Q9QV00	Q9qv00 rattus sp.
22	3	37.5	15	12	Q86576	Q86576 subterranea
23	3	37.5	16	4	Q9UCJ7	Q9ucj7 homo sapien
24	3	37.5	16	8	Q8HTT0	Q8htt0 columnea sp
25	3	37.5	16	8	Q8HTS9	Q8hts9 pinguicula
26	3	37.5	16	8	Q8HTS8	Q8hts8 pinguicula
27	3	37.5	16	8	Q8HTS7	Q8hts7 pinguicula
28	3	37.5	16	8	Q8HTS6	Q8hts6 utricularia
29	3	37.5	16	8	Q8HTS5	Q8hts5 utricularia
30	3	37.5	16	8	Q8HTS4	Q8hts4 utricularia
31	3	37.5	16	9	Q8H9Z9	Q8h9z9 bacterioph
32	3	37.5	16	15	Q75710	Q75710 human immun
33	3	37.5	17	2	Q9ZG32	Q9zg32 chlamydia t
34	3	37.5	17	2	P82586	P82586 streptococc
35	3	37.5	17	8	Q8HRZ4	Q8hrz4 ephedra sin
36	3	37.5	17	13	Q9DFB5	Q9dfb5 brachydanio
37	3	37.5	18	2	Q52411	Q52411 thermophili
38	3	37.5	18	4	Q16028	Q16028 homo sapien
39	3	37.5	18	8	Q9GE28	Q9ge28 amborella t
40	3	37.5	18	8	Q8HS04	Q8hs04 arabidopsis
41	3	37.5	19	2	Q9R517	Q9r517 mycobacteri
42	3	37.5	19	11	Q06028	Q06028 mus musculu

43	3	37.5	19	11	Q64132	Q64132 rattus sp.
44	3	37.5	19	11	Q922T5	Q922t5 mus musculu
45	3	37.5	20	2	Q9R5E2	Q9r5e2 aeromonas h

ALIGNMENTS

RESULT 1

O06946

ID O06946 PRELIMINARY; PRT; 17 AA.
AC O06946;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf238 (Fragment).
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=98036037; PubMed=9370270;
RA Hayes F., Lubetzki S.A., Sherratt D.J.;
RT "Salmonella typhimurium specifies a circular chromosome dimer
RT resolution system which is homologous to the Xer site-specific
RT recombination system of Escherichia coli.";
RL Gene 198:105-110(1997).
DR EMBL; U92525; AAC45779.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2072 MW; BEB65CE8F0F9F529 CRC64;

Query Match 50.0%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8
|||
Db 8 GRIC 11

RESULT 2

O32560

ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Propionate kinase (Fragment).
GN TDCD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hesslinger C., Sawers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of IS5 elements.";
RL DNA Seq. 9:183-188(1998).
DR EMBL; AJ001620; CAA04875.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RIC 8
|||
Db 4 RIC 6

RESULT 3

Q8MBF4

ID Q8MBF4 PRELIMINARY; PRT; 9 AA.
AC Q8MBF4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Ipomoea quamoclit.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=89660;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100854; AAM55540.1; -.
KW Chloroplast.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 961 MW; DD59440861B1AAAD CRC64;

Query Match 37.5%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 4

Q8MAZ9

ID Q8MAZ9 PRELIMINARY; PRT; 10 AA.
 AC Q8MAZ9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Dicranostyles ampla.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Dicranostyles.
 OX NCBI_TaxID=197378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100933; AAM55853.1; -.
 KW Chloroplast.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1074 MW; 836D59440861B1AA CRC64;

 Query Match 37.5%; Score 3; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 GRI 7
 |||
 Db 6 GRI 8

RESULT 5

Q8MBB7

ID Q8MBB7 PRELIMINARY; PRT; 10 AA.
 AC Q8MBB7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Merremia aegyptia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Merremia.
 OX NCBI_TaxID=197413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100875; AAM55624.1; -.
 KW Chloroplast.
 FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1074 MW; 836D59440861B1AA CRC64;

Query Match 37.5%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 6

Q8MAZ1

ID Q8MAZ1 PRELIMINARY; PRT; 11 AA.
AC Q8MAZ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Maripa paniculata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197411;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100937; AAM55869.1; -.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 7

Q8MB39

ID Q8MB39 PRELIMINARY; PRT; 11 AA.
AC Q8MB39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Wilsonia humilis.
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Wilsonia.
 OX NCBI_TaxID=197481;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100914; AAM55777.1; -.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 6 GRI 8

RESULT 8

Q8MB58

ID Q8MB58 PRELIMINARY; PRT; 11 AA.
 AC Q8MB58;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Seddera hirsuta.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Seddera.
 OX NCBI_TaxID=197444;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100905; AAM55743.1; -.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
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 Db 6 GRI 8

RESULT 9

Q8MAZ3

ID Q8MAZ3 PRELIMINARY; PRT; 11 AA.
 AC Q8MAZ3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Maripa repens.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Maripa.
 OX NCBI_TaxID=197412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100936; AAM55865.1; -.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 6 GRI 8

RESULT 10

Q8MBE1

ID Q8MBE1 PRELIMINARY; PRT; 11 AA.
 AC Q8MBE1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Ipomoea alba.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=89634;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";

RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100861; AAM55568.1; -.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 11

Q8MB77

ID Q8MB77 PRELIMINARY; PRT; 11 AA.
AC Q8MB77;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Odonellia hirtiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Convolvulaceae; Odonellia.
OX NCBI_TaxID=197424;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci."
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100897; AAM55711.1; -.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
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Qy 5 GRI 7
|||
Db 6 GRI 8

RESULT 12

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ID Q8MB79 PRELIMINARY; PRT; 11 AA.
AC Q8MB79;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE PsbJ (Fragment).
 GN PSBJ.
 OS Aniseia argentina.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Aniseia.
 OX NCBI_TaxID=197349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100895; AAM55703.1; -.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GRI 7
 |||
 Db 6 GRI 8

RESULT 13

Q8MB97

ID Q8MB97 PRELIMINARY; PRT; 11 AA.
 AC Q8MB97;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Merremia peltata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Convolvulaceae; Merremia.
 OX NCBI_TaxID=197416;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100885; AAM55663.1; -.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
Db 6 GRI 8

RESULT 14

Q31006

ID Q31006 PRELIMINARY; PRT; 12 AA.
AC Q31006;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bota protein (Fragment).
GN BOTA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052564; PubMed=1428011;
RA Ellis S.A., Braem K.A., Morrison W.I.;
RT "Transmembrane and cytoplasmic domain sequences demonstrate at least
RT two expressed bovine MHC class I loci.";
RL Immunogenetics 37:49-56(1992).
DR EMBL; S47738; AAB23972.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1306 MW; 6D9E2F805ABB5044 CRC64;

Query Match 37.5%; Score 3; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
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Db 4 GRI 6

RESULT 15

Q8MAX7

ID Q8MAX7 PRELIMINARY; PRT; 12 AA.
AC Q8MAX7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Tridynamia megalantha.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Convolvulaceae; Tridynamia.
OX NCBI_TaxID=197451;
RN [1]
RP SEQUENCE FROM N.A.

RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100945; AAM55900.1; -.
KW Chloroplast.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1316 MW; 92DAE36D59440861 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 6 GRI 8

Search completed: November 13, 2003, 10:38:16
Job time : 21.6667 secs

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:27:36 ; Search time 9 Seconds
 (without alignments)
 37.610 Million cell updates/sec

Title: US-09-228-866-8
 Perfect score: 8
 Sequence: 1 CLDWGRIC 8

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 118358

Minimum DB seq length: 7
 Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	8	100.0	8	1	US-08-526-710-8
2	8	100.0	8	3	US-08-862-855-8
3	8	100.0	8	3	US-09-226-985-8
4	8	100.0	8	4	US-09-227-906-8
5	6	75.0	8	1	US-08-526-710-7
6	6	75.0	8	3	US-08-862-855-7
7	6	75.0	8	3	US-09-226-985-7
8	6	75.0	8	4	US-09-227-906-7
9	5	62.5	10	2	US-08-733-505A-35
10	5	62.5	10	2	US-08-706-741B-70
11	5	62.5	10	2	US-08-924-695A-70

12	5	62.5	20	1	US-08-248-819A-39	Sequence 39, Appl
13	5	62.5	20	2	US-08-337-646A-57	Sequence 57, Appl
14	5	62.5	20	3	US-08-927-326-57	Sequence 57, Appl
15	5	62.5	21	1	US-08-112-208C-15	Sequence 15, Appl
16	5	62.5	21	1	US-08-248-819A-17	Sequence 17, Appl
17	5	62.5	21	2	US-08-337-646A-35	Sequence 35, Appl
18	5	62.5	21	2	US-08-856-531-15	Sequence 15, Appl
19	5	62.5	21	2	US-08-856-034-15	Sequence 15, Appl
20	5	62.5	21	3	US-08-927-326-35	Sequence 35, Appl
21	5	62.5	21	4	US-09-379-820A-15	Sequence 15, Appl
22	4	50.0	7	1	US-08-798-897-9	Sequence 9, Appli
23	4	50.0	7	2	US-08-978-523-9	Sequence 9, Appli
24	4	50.0	7	4	US-09-463-129B-6	Sequence 6, Appli
25	4	50.0	8	1	US-08-471-058-1	Sequence 1, Appli
26	4	50.0	8	3	US-08-471-057-1	Sequence 1, Appli
27	4	50.0	8	4	US-08-469-260A-528	Sequence 528, App
28	4	50.0	8	4	US-08-488-446-528	Sequence 528, App
29	4	50.0	8	4	US-08-470-865-1	Sequence 1, Appli
30	4	50.0	8	4	US-08-467-344A-528	Sequence 528, App
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34	4	50.0	10	2	US-08-706-741B-64	Sequence 64, Appl
35	4	50.0	10	2	US-08-924-695A-62	Sequence 62, Appl
36	4	50.0	10	2	US-08-924-695A-64	Sequence 64, Appl
37	4	50.0	11	2	US-08-733-505A-31	Sequence 31, Appl
38	4	50.0	11	2	US-08-733-505A-33	Sequence 33, Appl
39	4	50.0	11	2	US-08-706-741B-66	Sequence 66, Appl
40	4	50.0	11	2	US-08-706-741B-68	Sequence 68, Appl
41	4	50.0	11	2	US-08-924-695A-66	Sequence 66, Appl
42	4	50.0	11	2	US-08-924-695A-68	Sequence 68, Appl
43	4	50.0	13	1	US-08-248-819A-42	Sequence 42, Appl
44	4	50.0	13	1	US-08-248-819A-43	Sequence 43, Appl
45	4	50.0	13	1	US-08-798-897-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-08-526-710-8

; Sequence 8, Application US/08526710

; Patent No. 5622699

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Method of Identifying Molecules That

; TITLE OF INVENTION: Home to a Selected Organ In Vivo

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-8

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Query Match          100.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 CLDWGRIC 8
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Db      1 CLDWGRIC 8

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RESULT 2

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US-08-862-855-8
; Sequence 8, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-8

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Query Match          100.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 CLDWGRIC 8
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Db      1 CLDWGRIC 8

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RESULT 3

US-09-226-985-8

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; Sequence 8, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-8

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Query Match          100.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 CLDWGRIC 8
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Db      1 CLDWGRIC 8

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RESULT 4

US-09-227-906-8

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; Sequence 8, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-8

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Query Match          100.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 CLDWGRIC 8
        |||||
Db      1 CLDWGRIC 8

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RESULT 5

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US-08-526-710-7
; Sequence 7, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-7

Query Match 75.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8
| | | | |
Db 3 DWGRIC 8

RESULT 6

US-08-862-855-7

; Sequence 7, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-7

Query Match 75.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8
| | | | |
Db 3 DWGRIC 8

RESULT 7

US-09-226-985-7

; Sequence 7, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-7

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Query Match          75.0%; Score 6; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 DWGRIC 8
        |||||
Db      3 DWGRIC 8

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RESULT 8

US-09-227-906-7

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; Sequence 7, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-7

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```

Query Match          75.0%; Score 6; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      3 DWGRIC 8
        |||||
Db      3 DWGRIC 8

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RESULT 9

US-08-733-505A-35

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; Sequence 35, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197

```

; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-35

Query Match 62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 5 WGRIC 9

RESULT 10

US-08-706-741B-70

; Sequence 70, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-706-741B-70

Query Match 62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 5 WGRIC 9

RESULT 11

US-08-924-695A-70
; Sequence 70, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-695A-70

Query Match 62.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 |||||
Db 5 WGRIC 9

RESULT 12

US-08-248-819A-39

; Sequence 39, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:

US-08-248-819A-39

Query Match 62.5%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
| | | | |
Db 9 WGRIC 13

RESULT 13

US-08-337-646A-57

; Sequence 57, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:
US-08-337-646A-57

Query Match 62.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
| | | |
Db 9 WGRIC 13

RESULT 14

US-08-927-326-57

; Sequence 57, Application US/08927326

; Patent No. 6184202

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, Stanley J.

; TITLE OF INVENTION: CELL DEATH REGULATORS

; NUMBER OF SEQUENCES: 78

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/927,326

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/337,646

; FILING DATE: 10-NOV-1994

; APPLICATION NUMBER: US 08/248,819

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/112,208

; FILING DATE: 26-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15726A-000620

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 4
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:
US-08-927-326-57

Query Match 62.5%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 9 WGRIC 13

RESULT 15

US-08-112-208C-15

; Sequence 15, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "Amino acid is either K
; OTHER INFORMATION:

US-08-112-208C-15

Query Match 62.5%; Score 5; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
|||||
Db 10 WGRIC 14

Search completed: November 13, 2003, 10:41:56
Job time : 9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:53:11 ; Search time 25.6667 Seconds
(without alignments)
49.473 Million cell updates/sec

Title: US-09-228-866-8
Perfect score: 8
Sequence: 1 CLDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

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Total number of hits satisfying chosen parameters: 358712

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		Length	DB	ID	Description
	No.	Score				
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2	8	100.0	8	21	AAB07394	Brain homing pepti
3	8	100.0	8	22	AAE11800	Phage peptide #8 t
4	8	100.0	8	23	AAU10711	Brain homing pepti
5	6	75.0	8	18	AAW13418	Brain homing pepti
6	6	75.0	8	21	AAB07393	Brain homing pepti
7	6	75.0	8	22	AAE11799	Phage peptide #7 t
8	6	75.0	8	23	AAU10710	Brain homing pepti
9	5	62.5	20	22	AAB74174	LMW5-HL BH1 domain
10	5	62.5	21	20	AAW87835	Bcl-2 related prot
11	5	62.5	21	22	AAB74152	LMW5-HL BH1 domain
12	4	50.0	7	20	AAW97429	Shigella-like toxi
13	4	50.0	8	21	AAB09401	Hepatitis GB virus
14	4	50.0	10	20	AAW95550	Peptide 10 from Bc
15	4	50.0	10	22	AAG97002	Human complementar
16	4	50.0	12	22	AAB70476	Bcl-2 protein Bcl-
17	4	50.0	12	22	AAB70478	Bcl-x protein Bcl-
18	4	50.0	13	22	AAB74177	Wild-type BCL2 BH1
19	4	50.0	13	22	AAB74178	BCL2 BH1 domain mu
20	4	50.0	14	21	AAW65535	Oestrogen receptor
21	4	50.0	14	23	AAU86272	Oestrogen receptor
22	4	50.0	15	19	AAW62156	Agrobacterium faec
23	4	50.0	15	20	AAW87842	Human Bcl-2 domain
24	4	50.0	15	20	AAW87843	Human Bcl-2 domain
25	4	50.0	15	22	AAB74159	Wild-type BCL2 BH1
26	4	50.0	15	22	AAB74160	BCL2 BH1 domain mu
27	4	50.0	15	24	ABP71851	Human EDF-1 protei
28	4	50.0	17	23	ABG62314	Eubacterial DNA po
29	4	50.0	18	22	ABB45281	Rabbit albumin-bin
30	4	50.0	20	19	AAW56780	Human wild-type BC
31	4	50.0	20	19	AAW56781	Human wild-type BC
32	4	50.0	20	20	AAW87820	Epitope of a Bcl-2
33	4	50.0	20	21	AAB19501	Bcl-2 BH1 domain.
34	4	50.0	20	21	AAB19502	Bcl-XL BH1 domain.
35	4	50.0	20	22	AAB74137	Bax epitope #7. U
36	4	50.0	20	22	AAB74169	BCL2 BH1 domain #2
37	4	50.0	20	22	AAB74171	BCL-XL BH1 domain.
38	4	50.0	21	22	AAB74149	BCL2 BH1 domain #1
39	4	50.0	21	22	AAB74172	MCL-1 BH1 domain.
40	4	50.0	21	22	AAB74173	A1 BH1 domain. Mu
41	3	37.5	7	16	AAR72750	Antimalarial pepti
42	3	37.5	7	16	AAR72754	Antimalarial pepti
43	3	37.5	7	16	AAR72758	Antimalarial pepti
44	3	37.5	7	16	AAR72762	Antimalarial pepti
45	3	37.5	7	16	AAR72585	EMAPII active pept

ALIGNMENTS

RESULT 1

AAW13419

ID AAW13419 standard; Peptide; 8 AA.

XX

AC AAW13419;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;

KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in

PT vivo panning method, specifically to identify brain, kidney,

PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 15; Page 68; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing
 CC peptide that was identified using a novel method for obtaining
 CC molecules that home to a selected organ or tissue. This in vivo
 CC panning method typically involves administering a phage display
 CC library to a subject, and identifying expressed peptides which
 CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
 CC vascular tissue or tumour tissue. The isolated peptides (see
 CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
 CC labels to the selected organ/tissue (claimed) or to identify and/or
 CC isolate target molecules (claimed). The peptides can be directly
 CC identified in vivo, as compared to prior art in vitro screening
 CC methods, which require further examination to see if they maintain
 CC specificity in vivo.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 18; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDWGRIC 8

Db

|||||||
1 CLDWGRIC 8

RESULT 2

AAB07394

ID AAB07394 standard; peptide; 8 AA.

XX

AC AAB07394;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 8.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..8

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in
PT vivo panning comprises administering a library of diverse peptides
PT linked to a tag which facilitates recovery of these peptides -

XX

PS Example 2; Column 17; 20pp; English.

XX

CC The present sequence is a mouse brain homing peptide. This sequence was
CC identified by using in vivo panning to screen a library of potential
CC organ homing molecules. The present sequence can be used to direct a
CC moiety to a the brain tissue, by linking the moiety to the present
CC sequence. Examples of potential moieties are drugs, toxins or a
CC detectable label. The present sequence contains a DXXR amino acid motif
CC (AAB12027). The DXXR motif resembles the RGD, DGR and NGR motifs that
CC bind to certain integrins.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDWGRIC 8
 |||||||
Db 1 CLDWGRIC 8

RESULT 3

AAE11800

ID AAE11800 standard; peptide; 8 AA.

XX

AC AAE11800;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #8 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo
PT panning that selectively home to a selected organ or tissue useful for
PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 8 AA;

Query Match

100.0%; Score 8; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDWGRIC 8
 |||||||
Db 1 CLDWGRIC 8

RESULT 4

AAU10711

ID AAU10711 standard; peptide; 8 AA.

XX

AC AAU10711;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #8 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;

KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.

XX

PT Recovering molecules that home to an organ or tissue, useful for
PT identifying molecules that home to a specific organ or tissue, e.g.
PT identifying a tumour homing molecule to identify the presence of cancer,
PT by in vivo panning of a library -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering
CC to the subject the library of diverse molecules, collecting a sample of
CC the selected organ or tissue (e.g. brain or kidney), and recovering from
CC the sample several molecules that home to the selected organ or tissue.
CC The method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety
CC (e.g. drug, toxin or detectable label) to the selected organ.
CC Specifically, the method is useful for identifying the presence of cancer

CC in a subject by linking an appropriate moiety to a tumour homing
CC molecule. The present method provides a direct means for identifying
CC molecules that specifically home to a selected organ and, therefore
CC provides a significant advantage over previous methods, which require
CC that a molecule identified using an in vitro screening method
CC subsequently be examined to determine if it maintains its specificity in
CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
CC the present invention.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDWGRIC 8
|||
Db 1 CLDWGRIC 8

RESULT 5

AAW13418

ID AAW13418 standard; Peptide; 8 AA.

XX

AC AAW13418;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;
KW drug delivery.

XX

OS Synthetic.

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in
PT vivo panning method, specifically to identify brain, kidney,
PT angiogenic vasculature or tumour tissue homing peptide(s)

XX

PS Claim 15; Page 68; 75pp; English.

XX

CC This synthetic peptide is a claimed example of a brain-homing

CC peptide that was identified using a novel method for obtaining
 CC molecules that home to a selected organ or tissue. This in vivo
 CC panning method typically involves administering a phage display
 CC library to a subject, and identifying expressed peptides which
 CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic
 CC vascular tissue or tumour tissue. The isolated peptides (see
 CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or
 CC labels to the selected organ/tissue (claimed) or to identify and/or
 CC isolate target molecules (claimed). The peptides can be directly
 CC identified in vivo, as compared to prior art in vitro screening
 CC methods, which require further examination to see if they maintain
 CC specificity in vivo.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 6

AAB07393

ID AAB07393 standard; peptide; 8 AA.

XX

AC AAB07393;

XX

DT 17-OCT-2000 (first entry)

XX

DE Brain homing peptide # 7.

XX

KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..8

FT /note= "Can optionally form a cyclic peptide"

XX

PN US6068829-A.

XX

PD 30-MAY-2000.

XX

PF 23-JUN-1997; 97US-0862855.

XX

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 2000-410850/35.

XX

PT Identifying and recovering organ homing molecules or peptides by in
PT vivo panning comprises administering a library of diverse peptides
PT linked to a tag which facilitates recovery of these peptides -

XX

PS Example 2; Column 17; 20pp; English.

XX

CC The present sequence is a mouse brain homing peptide. This sequence was
CC identified by using in vivo panning to screen a library of potential
CC organ homing molecules. The present sequence can be used to direct a
CC moiety to a the brain tissue, by linking the moiety to the present
CC sequence. Examples of potential moieties are drugs, toxins or a
CC detectable label. The present sequence contains a DXXR amino acid motif
CC (AAB12027). The DXXR motif resembles the RGD, DGR and NGR motifs that
CC bind to certain integrins.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 7

AAE11799

ID AAE11799 standard; peptide; 8 AA.

XX

AC AAE11799;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #7 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo
PT panning that selectively home to a selected organ or tissue useful for
PT treating disease or in diagnostic methods -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing
CC molecules that selectively home to a selected organ or tissue such as
CC brain, kidney or tumour recovered by in vivo panning. The invention
CC generally relates to the field of molecular medicine, drug delivery and
CC to a method of invivo panning for identifying a molecule that homes to a
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins
CC and fragments of proteins contained in an enriched library fraction may
CC be administered to a subject as part of a pharmaceutical composition to
CC treat disease or in diagnostic methods. The present sequence is a
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 8

AAU10710

ID AAU10710 standard; peptide; 8 AA.

XX

AC AAU10710;

XX

DT 12-MAR-2002 (first entry)

XX

DE Brain homing peptide #7 useful for delivery of target molecules.

XX

KW Organ targeting; tissue targeting; cancer; tumour homing molecule;
KW delivery of target molecule; brain homing peptide.

XX

OS Synthetic.

XX

PN US6306365-B1.

XX

PD 23-OCT-2001.

XX

PF 08-JAN-1999; 99US-0227906.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2002-040196/05.

XX

PT Recovering molecules that home to an organ or tissue, useful for
PT identifying molecules that home to a specific organ or tissue, e.g.
PT identifying a tumour homing molecule to identify the presence of cancer,
PT by in vivo panning of a library -

XX

PS Example 2; Column 17; 21pp; English.

XX

CC The present invention relates to a method of recovering molecules that
CC home to a selected organ or tissue. The method comprises administering
CC to the subject the library of diverse molecules, collecting a sample of
CC the selected organ or tissue (e.g. brain or kidney), and recovering from
CC the sample several molecules that home to the selected organ or tissue.
CC The method is useful for identifying molecules, particularly useful for
CC screening large number of molecules (e.g. peptides), that home to a
CC specific organ. The identified molecule is useful for e.g. raising an
CC antibody specific for a target molecule, targeting a desired moiety
CC (e.g. drug, toxin or detectable label) to the selected organ.
CC Specifically, the method is useful for identifying the presence of cancer
CC in a subject by linking an appropriate moiety to a tumour homing
CC molecule. The present method provides a direct means for identifying
CC molecules that specifically home to a selected organ and, therefore
CC provides a significant advantage over previous methods, which require
CC that a molecule identified using an in vitro screening method
CC subsequently be examined to determine if it maintains its specificity in
CC vivo. AAU10704-AAU10723 represent brain homing peptides described in
CC the present invention.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 6; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGRIC 8

|||||

Db 3 DWGRIC 8

RESULT 9

AAB74174

ID AAB74174 standard; Peptide; 20 AA.

XX

AC AAB74174;

XX

DT 22-MAY-2001 (first entry)

XX

DE LMW5-HL BH1 domain #2.

XX

KW Bax; cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischaemia; Bcl-2;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.

XX

OS Unidentified.
 XX
 PN US6184202-B1.
 XX
 PD 06-FEB-2001.
 XX
 PF 11-SEP-1997; 97US-0927326.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 2001-256104/26.
 XX
 PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
 PT adult tissues, or treating proliferative or autoimmune diseases,
 PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
 PT bcl-2 associated X protein -
 XX
 PS Example 11; Fig 22; 105pp; English.
 XX
 CC The present invention relates to a method of modulating apoptosis of a
 CC cell. The method comprises administering to the cell an agent,
 CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
 CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
 CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
 CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
 CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
 CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
 CC traumatic brain injury, neurodegenerative diseases, aging, ischaemia,
 CC toxemia, infection, hepatitis, transplant rejection, and
 CC lymphoproliferative diseases. The present sequence is a peptide, which
 CC was used in the method of the present invention.
 XX
 SQ Sequence 20 AA;

Query Match 62.5%; Score 5; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 |||||
 Db 9 WGRIC 13

RESULT 10
 AAW87835
 ID AAW87835 standard; Peptide; 21 AA.
 XX
 AC AAW87835;
 XX
 DT 10-MAR-1999 (first entry)
 XX

DE Bcl-2 related protein (LMW5-HL) domain BH1 peptide.
 XX
 KW Bcl-2 related protein; Bax; bcl-2; modulator; domain BH1;
 KW bcl-2-related function; apoptosis; dimer; Bcl-xL; Mcl-1; A1.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "Arg or Lys"
 XX
 PN US5856171-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 10-NOV-1994; 94US-0337646.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 1999-105119/09.
 XX
 PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
 PT identifying modulators of bcl-2 function
 XX
 PS Example 10; Fig 14A; 105pp; English.
 XX
 CC AAW87832-36 represent the amino acid sequences of domain BH1 of
 CC Bcl-2-related proteins. The specification describes a composition
 CC comprising a hybrid protein comprising an activator domain of a
 CC transcriptional activator protein and a bcl-2 family member having
 CC a BH1 domain and a BH2 domain; another hybrid protein comprising a
 CC DNA-binding domain of the transcriptional activator protein and a
 CC second bcl-2 family member having a BH1 domain and a BH2 domain; and
 CC a reporter gene linked to a transcriptional regulatory element whose
 CC transcriptional activity is dependent on the presence or absence of
 CC a dimer of the two hybrid proteins. The bcl-2 family members are
 CC selected from naturally occurring Bcl-2, Bcl-xL, Bax, Mcl-1, A1,
 CC fragments thereof, and mutants having a mutation in the BH1 and/or
 CC BH2 domain that alters intermolecular binding of the two bcl-2 family
 CC members. The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2, which
 CC would be potentially useful as drugs for modulating apoptosis.
 XX
 SQ Sequence 21 AA;

Query Match 62.5%; Score 5; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8
 |||||

RESULT 11

AAB74152

ID AAB74152 standard; Peptide; 21 AA.

XX

AC AAB74152;

XX

DT 22-MAY-2001 (first entry)

XX

DE LMW5-HL BH1 domain #1.

XX

KW Bax; cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischaemia; Bcl-2;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.

XX

OS Unidentified.

XX

PN US6184202-B1.

XX

PD 06-FEB-2001.

XX

PF 11-SEP-1997; 97US-0927326.

XX

PR 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Korsmeyer SJ;

XX

DR WPI; 2001-256104/26.

XX

PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
PT adult tissues, or treating proliferative or autoimmune diseases,
PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
PT bcl-2 associated X protein -

XX

PS Example 10; Fig 14; 105pp; English.

XX

CC The present invention relates to a method of modulating apoptosis of a
CC cell. The method comprises administering to the cell an agent,
CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
CC traumatic brain injury, neurodegenerative diseases, aging, ischaemia,
CC toxemia, infection, hepatitis, transplant rejection, and
CC lymphoproliferative diseases. The present sequence is a peptide, which
CC was used in the method of the present invention.

XX

SQ Sequence 21 AA;

Query Match 62.5%; Score 5; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRIC 8

|||||

Db 10 WGRIC 14

RESULT 12

AAW97429

ID AAW97429 standard; peptide; 7 AA.

XX

AC AAW97429;

XX

DT 19-MAY-1999 (first entry)

XX

DE Shigella-like toxin epitope from Escherichia coli O157:H7.

XX

KW Shigella-like toxin; SLT; Escherichia coli O157:H7;
KW epitope; vaccine.

XX

OS Escherichia coli.

XX

PN WO9905169-A1.

XX

PD 04-FEB-1999.

XX

PF 17-JUL-1998; 98WO-GB02156.

XX

PR 21-JUL-1997; 97GB-0015177.

XX

PA (NEUT-) NEUTEC PHARMA PLC.

XX

PI Burnie JP, Matthews RC;

XX

DR WPI; 1999-142851/12.

XX

PT New epitopes of shigella-like toxin (SLT) - useful in the diagnosis
PT and treatment of pathogens expressing SLTs, particularly E. coli
PT O157:H7

XX

PS Claim 1; Page 21; 29pp; English.

XX

CC AAW97424-30 represents epitope of shigella-like toxin (SLT) from
CC Escherichia coli O157:H7. The epitopes and their binding agents
CC are used in the diagnosis and treatment of animals or humans.
CC The epitopes can be used as an immunogen or vaccine.

XX

SQ Sequence 7 AA;

Query Match 50.0%; Score 4; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 1 WGRI 4

RESULT 13

AAB09401

ID AAB09401 standard; Protein; 8 AA.

XX

AC AAB09401;

XX

DT 30-AUG-2000 (first entry)

XX

DE Hepatitis GB virus protein sequence SEQ ID NO:528.

XX

KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
KW infection; detection; characterisation; hepatitis.

XX

OS Hepatitis GB virus.

XX

PN US6051374-A.

XX

PD 18-APR-2000.

XX

PF 07-JUN-1995; 95US-0488445.

XX

PR 14-FEB-1994; 94US-0196030.

PR 13-MAY-1994; 94US-0242654.

PR 29-JUL-1994; 94US-0283314.

PR 23-NOV-1994; 94US-0344185.

PR 23-NOV-1994; 94US-0344190.

PR 30-JAN-1995; 95US-0377557.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;

XX

DR WPI; 2000-338307/29.

XX

PT Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the
PT HGBV polynucleotide probe and detecting the complex that contains
PT target HGBV -

XX

PS Example 18; Column 539-540; 369pp; English.

XX

CC The present invention describe a method for detecting target
CC hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T)
CC suspected of containing HGBV. The method involves reacting (T) with a
CC HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and
CC which selectively hybridises to the HGBV genome or its full complement,
CC and detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid
CC in the test sample suspected of containing HGBV and for characterisation
CC of newly ascertained etiological agent of non-A, non-B, non-C, non-D and

CC non-E hepatitis causing agents collectively termed as hepatitis GB
CC virus. AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide
CC and protein sequences used in the exemplification of the present
CC invention.

XX

SQ Sequence 8 AA;

Query Match 50.0%; Score 4; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDW 4

||||

Db 2 CLDW 5

RESULT 14

AAW95550

ID AAW95550 standard; peptide; 10 AA.

XX

AC AAW95550;

XX

DT 26-MAR-1999 (first entry)

XX

DE Peptide 10 from Bcl-2-related family.

XX

KW Cytochrome C; apoptotic; Bcl-2; neurodegeneration; Bcl-xL; cancer;
KW autoimmune disease; rheumatoid arthritis; transplant rejection; AIDS;
KW insulin-dependent diabetes mellitus.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9858541-A1.

XX

PD 30-DEC-1998.

XX

PF 16-JUN-1998; 98WO-US12595.

XX

PR 24-JUN-1997; 97US-0881646.

XX

PA (DAND) DANA FARBER CANCER INST INC.

PA (NOVS) NOVARTIS AG.

XX

PI Kharbanda SM, Kufe DW, Nalin CM, Sharma SK;

XX

DR WPI; 1999-080967/07.

XX

PT New peptides that inhibit binding of cytochrome C to anti-apoptotic
PT Bcl-2 proteins - useful in the treatment of autoimmune disease,
PT transplant rejection and cancer, and also in screening for
PT modulators of apoptosis

XX

PS Example 3; Page 14; 64pp; English.

XX

CC The invention relates to a peptide that inhibits binding of cytochrome C
CC to an anti-apoptotic member of the Bcl-2 family. The peptides are used

CC to screen for compounds that promote or inhibit apoptosis (for treating
 CC neurodegeneration). The peptides, or peptidomimetics, are used to
 CC inhibit binding of cytochrome C to Bcl-xL in mammalian cells. This is
 CC used to treat autoimmune diseases (e.g. rheumatoid arthritis or
 CC insulin-dependent diabetes mellitus), transplant rejection and cancer,
 CC optionally in combination with chemotherapy, radiotherapy or
 CC immunotherapy. Nucleic acid encoding polypeptides that include the
 CC peptide (AAW95539-42) sequences is used to inhibit release of cytochrome
 CC C into the cytosol, specifically in patients with acquired immune
 CC deficiency syndrome, and also to promote survival of haematopoietic cells
 CC in patients undergoing chemo- or radio- therapy. Antibodies that bind
 CC specifically to an epitope in peptides AAW95539-42 are used to determine
 CC Bcl-xL or Bcl-2, for diagnosis or prognosis, and also in screening
 CC assays. Administration of the peptides in targeting vehicles may
 CC eliminate specific pathogenic cells without harming the rest of the
 CC immune system. Sequences AAW95543-52 represents peptide fragments from
 CC Bcl-2-related family that were used in assays for inhibition of binding
 CC of fused GST-Bcl-xL to cytochrome C

XX

SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7

||||

Db 4 WGRI 7

RESULT 15

AAG97002

ID AAG97002 standard; Peptide; 10 AA.

XX

AC AAG97002;

XX

DT 18-SEP-2001 (first entry)

XX

DE Human complementary peptide, SEQ ID NO: 3196.

XX

KW Human; complementary peptide; ligand; drug discovery; drug design.

XX

OS Homo sapiens.

XX

PN WO200142277-A2.

XX

PD 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-GB04776.

XX

PR 13-DEC-1999; 99GB-0029464.

XX

PA (PROT-) PROTEOM LTD.

XX

PI Roberts GW, Heal JR;

XX

DR WPI; 2001-408419/43.

XX
PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -

XX
PS Example 4; Page 503; 646pp; English.

XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.

XX
SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8
||||
Db 7 GRIC 10

Search completed: November 13, 2003, 10:32:56
Job time : 26.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:38:27 ; Search time 15.6667 Seconds
(without alignments)
93.222 Million cell updates/sec

Title: US-09-228-866-8
Perfect score: 8
Sequence: 1 CLDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 124183

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	62.5	21	15	US-10-277-693A-15	Sequence 15, Appl
2	4	50.0	8	8	US-08-424-550B-528	Sequence 528, App
3	4	50.0	8	15	US-10-101-482-1	Sequence 1, Appli
4	4	50.0	10	11	US-09-572-404B-3196	Sequence 3196, Ap
5	4	50.0	15	15	US-10-277-693A-22	Sequence 22, Appl
6	4	50.0	15	15	US-10-277-693A-23	Sequence 23, Appl
7	4	50.0	17	12	US-10-280-066-83	Sequence 83, Appl
8	4	50.0	18	11	US-09-539-443-52	Sequence 52, Appl
9	4	50.0	20	10	US-09-990-385-4	Sequence 4, Appli
10	4	50.0	21	15	US-10-277-693A-12	Sequence 12, Appl
11	3	37.5	7	10	US-09-859-214-10	Sequence 10, Appl
12	3	37.5	7	10	US-09-851-026-3	Sequence 3, Appli
13	3	37.5	7	10	US-09-851-026-9	Sequence 9, Appli
14	3	37.5	7	10	US-09-851-026-10	Sequence 10, Appl
15	3	37.5	7	10	US-09-851-026-37	Sequence 37, Appl
16	3	37.5	7	10	US-09-813-718-26	Sequence 26, Appl
17	3	37.5	7	10	US-09-813-718-27	Sequence 27, Appl
18	3	37.5	7	10	US-09-813-718-31	Sequence 31, Appl
19	3	37.5	7	10	US-09-813-718-33	Sequence 33, Appl
20	3	37.5	7	10	US-09-884-767A-18	Sequence 18, Appl
21	3	37.5	7	11	US-09-847-946A-37	Sequence 37, Appl
22	3	37.5	7	11	US-09-847-946A-66	Sequence 66, Appl
23	3	37.5	7	11	US-09-847-946A-110	Sequence 110, App
24	3	37.5	7	11	US-09-847-946A-121	Sequence 121, App
25	3	37.5	7	12	US-10-300-699-46	Sequence 46, Appl
26	3	37.5	7	12	US-10-257-050-12	Sequence 12, Appl
27	3	37.5	7	12	US-10-319-402-8	Sequence 8, Appli
28	3	37.5	7	12	US-10-319-402-10	Sequence 10, Appl

29	3	37.5	7	15	US-10-006-869-2720	Sequence 2720, Ap
30	3	37.5	7	15	US-10-006-869-3652	Sequence 3652, Ap
31	3	37.5	8	11	US-09-847-946A-30	Sequence 30, Appl
32	3	37.5	8	11	US-09-847-946A-38	Sequence 38, Appl
33	3	37.5	8	11	US-09-847-946A-59	Sequence 59, Appl
34	3	37.5	8	11	US-09-847-946A-67	Sequence 67, Appl
35	3	37.5	8	11	US-09-847-946A-103	Sequence 103, App
36	3	37.5	8	11	US-09-847-946A-111	Sequence 111, App
37	3	37.5	8	11	US-09-847-946A-114	Sequence 114, App
38	3	37.5	8	11	US-09-847-946A-122	Sequence 122, App
39	3	37.5	8	11	US-09-880-748-2982	Sequence 2982, Ap
40	3	37.5	8	11	US-09-972-656-62	Sequence 62, Appl
41	3	37.5	8	12	US-10-348-504-70	Sequence 70, Appl
42	3	37.5	8	12	US-10-348-504-71	Sequence 71, Appl
43	3	37.5	8	12	US-10-348-504-72	Sequence 72, Appl
44	3	37.5	8	12	US-10-348-504-73	Sequence 73, Appl
45	3	37.5	8	12	US-10-348-504-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1

US-10-277-693A-15

```

; Sequence 15, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Amino acid is either K (Lys) or R (Arg)
US-10-277-693A-15

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Query Match          62.5%;  Score 5;  DB 15;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 17;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy 4 WGRIC 8
 |||||
Db 10 WGRIC 14

RESULT 2

US-08-424-550B-528

; Sequence 528, Application US/08424550B

; Publication No. US20020119447A1

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,550B

; FILING DATE:

; CLASSIFICATION: 435435

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 528:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-424-550B-528

Query Match 50.0%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLDW 4
 ||||
Db 2 CLDW 5

RESULT 3

US-10-101-482-1

; Sequence 1, Application US/10101482

; Publication No. US20030008837A1

; GENERAL INFORMATION:

; APPLICANT: KIEFER, MICHAEL C.

; BARR, PHILIP J.

; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA

; ENCODING THE PROTEINS AND METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,482

; FILING DATE: 18-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/320,157

; FILING DATE: 07-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: LEHNHARDT, SUSAN K.

; REGISTRATION NUMBER: 33,943

; REFERENCE/DOCKET NUMBER: 23647-20007.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-101-482-1

Query Match 50.0%; Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWGR 6
 ||||
Db 1 DWGR 4

RESULT 4

US-09-572-404B-3196
; Sequence 3196, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3196
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERBB3 OR HER3 at 523-532 and may
interact with
; OTHER INFORMATION: Sequence 3195 in this patent.
US-09-572-404B-3196

Query Match 50.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRIC 8
 ||||
Db 7 GRIC 10

RESULT 5

US-10-277-693A-22
; Sequence 22, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT

; ORGANISM: Murine
US-10-277-693A-22

Query Match 50.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 10 WGRI 13

RESULT 6

US-10-277-693A-23
; Sequence 23, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Murine
US-10-277-693A-23

Query Match 50.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGRI 7
|||
Db 10 WGRI 13

RESULT 7

US-10-280-066-83
; Sequence 83, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.

```

; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING
TARGET BINDERS
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: DGI-2-20R-4-G22
US-10-280-066-83

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Query Match          50.0%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      3 DWGR 6
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Db      6 DWGR 9

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RESULT 8

US-09-539-443-52

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; Sequence 52, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-539-443-52

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Query Match          50.0%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      5 GRIC 8
        ||||
Db      3 GRIC 6

```

RESULT 9

US-09-990-385-4

; Sequence 4, Application US/09990385

; Publication No. US20020192771A1

; GENERAL INFORMATION:

; APPLICANT: Koji YANAI et al.

; TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF

; ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR
PRODUCING

; BETA-FRUCTOFURANOSIDASE, AND BETA-
FRUCTOFURANOSIDASE VARIANT

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

; STREET: 2033 K Street, N.W., Suite 800

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/990,385

; FILING DATE: 10-Sep-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/142,623

; FILING DATE: September 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee Cheng

; REGISTRATION NUMBER: 40,949

```

; REFERENCE/DOCKET NUMBER: 2001-1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acid residues
; TYPE: Amino acid
; STRANDEDNESS: No. US20020192771A1 relevant
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Microorganism: Aspergillus niger ACE-2-1
; (ATCC 20611)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-990-385-4

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Query Match          50.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      2 LDWG 5
        ||||
Db      11 LDWG 14

```

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RESULT 10
US-10-277-693A-12
; Sequence 12, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Murine
US-10-277-693A-12

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Query Match          50.0%; Score 4; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      4 WGRI 7
        ||||

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RESULT 11

US-09-859-214-10

; Sequence 10, Application US/09859214

; Patent No. US20020103111A1

; GENERAL INFORMATION:

; APPLICANT: Schwender, Charles F.

; Shroff, Hitesh N.

; TITLE OF INVENTION: INHIBITORS OF MadCAM-1-MEDIATED

; INTERACTIONS AND METHODS OF USE THEREFOR

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02421

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/859,214

; FILING DATE: 16-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/109,879

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/582,740

; FILING DATE: 04-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: LKS95-12A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781) 861-6240

; TELEFAX: (781) 861-9540

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: circular

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /label= modified aa

; /note= "Ac - Cysteine"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 7

; OTHER INFORMATION: /label= Modified aa

; /note= "cysteine - NH2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-859-214-10

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLD 3
|||
Db 1 CLD 3

RESULT 12

US-09-851-026-3

; Sequence 3, Application US/09851026

; Patent No. US20020160957A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; Clauss, Matthias

; Kao, Janet

; Kayton, Mark

; Libutti, Steven K

; TITLE OF INVENTION: Endothelial Monocyte Activating

; Polypeptide II: A Mediator Which Activates Host

Response

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham, LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.30, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/851,026

; FILING DATE: 07-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,821

; FILING DATE: 08-OCT-96

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-851-026-3

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 3 GRI 5

RESULT 13

US-09-851-026-9

; Sequence 9, Application US/09851026
; Patent No. US20020160957A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K

; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host

Response

; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: Peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-851-026-9

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
Db 3 GRI 5

RESULT 14

US-09-851-026-10

; Sequence 10, Application US/09851026

; Patent No. US20020160957A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; Clauss, Matthias

; Kao, Janet

; Kayton, Mark

; Libutti, Steven K

; TITLE OF INVENTION: Endothelial Monocyte Activating

; Polypeptide II: A Mediator Which Activates Host

Response

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham, LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.30, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/851,026

; FILING DATE: 07-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,821

; FILING DATE: 08-OCT-96

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-851-026-10

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 3 GRI 5

RESULT 15

US-09-851-026-37

; Sequence 37, Application US/09851026

; Patent No. US20020160957A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; Clauss, Matthias

; Kao, Janet

; Kayton, Mark

; Libutti, Steven K

; TITLE OF INVENTION: Endothelial Monocyte Activating

; Polypeptide II: A Mediator Which Activates Host

Response

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham, LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.30, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/851,026

; FILING DATE: 07-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,821

; FILING DATE: 08-OCT-96

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-851-026-37

Query Match 37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 2 GRI 4

Search completed: November 13, 2003, 11:12:33
Job time : 15.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 10:26:01 ; Search time 7.83333 Seconds
(without alignments)
98.215 Million cell updates/sec

Title: US-09-228-866-8
Perfect score: 8
Sequence: 1 CLDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3752

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	37.5	7	2	PT0628	T-cell receptor be	
2	3	37.5	7	2	PT0642	T-cell receptor be	
3	3	37.5	7	2	PT0722	T-cell receptor be	
4	3	37.5	7	2	PT0728	T-cell receptor be	
5	3	37.5	8	2	PT0724	T-cell receptor be	
6	3	37.5	10	2	A40753	aldehyde ferredoxi	
7	3	37.5	10	2	PH1344	Ig heavy chain DJ	
8	3	37.5	10	2	PH0923	T-cell receptor be	
9	3	37.5	12	2	I46922	gene Bota protein	
10	3	37.5	13	2	PH0928	T-cell receptor be	
11	3	37.5	15	2	I46512	troponin - rabbit	
12	3	37.5	15	2	JT0610	leukocyte chemoatt	
13	3	37.5	15	2	S60007	glial hyaluronate-	
14	3	37.5	17	2	I46511	troponin - rabbit	
15	3	37.5	17	2	I67526	CD33 antigen homol	
16	3	37.5	18	2	S49026	ribosomal protein	
17	3	37.5	18	2	B61110	68K collagen-bindi	
18	3	37.5	19	2	A28814	Ig kappa chain V r	
19	3	37.5	19	2	S12268	Qa-2 antigen - mou	
20	3	37.5	19	2	I49037	TcR delta chain V-	
21	3	37.5	20	2	C54052	phosphoribosyl-AMP	
22	3	37.5	20	2	S65399	immunodeficiency v	
23	3	37.5	20	2	PC4384	DnaK protein homol	
24	3	37.5	20	2	S28435	major outer membra	
25	3	37.5	20	2	PQ0071	T-cell receptor be	
26	3	37.5	21	2	B12055	glyceraldehyde-3-p	
27	2	25.0	7	2	S16364	opacity protein P.	
28	2	25.0	7	2	S16365	opacity protein P.	
29	2	25.0	7	2	S57274	triacylglycerol li	
30	2	25.0	7	2	C56793	platelet glycoprot	
31	2	25.0	7	2	PT0526	T-cell receptor be	
32	2	25.0	7	2	PT0667	T-cell receptor be	
33	2	25.0	7	2	PT0655	T-cell receptor be	
34	2	25.0	7	2	PT0688	T-cell receptor be	
35	2	25.0	7	2	PT0586	T-cell receptor be	
36	2	25.0	7	2	B48394	major fat-globule	
37	2	25.0	7	2	PD0029	pev-kinin 1 - pena	
38	2	25.0	7	2	S09066	globulin IV alpha	
39	2	25.0	8	2	S15422	adipokinetic hormo	
40	2	25.0	8	2	S11545	adipokinetic hormo	
41	2	25.0	8	2	A58641	adipokinetic hormo	
42	2	25.0	8	2	E60588	sperm-activating p	
43	2	25.0	8	2	G60588	sperm-activating p	
44	2	25.0	8	2	A31570	angiotensin-conver	
45	2	25.0	8	2	S70727	ipqF protein - Shi	

ALIGNMENTS

RESULT 1

PT0628

T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0628

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0628

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 5 DWG 7

RESULT 2

PT0642

T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0642

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0642

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 4 DWG 6

RESULT 3

PT0722

T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0722

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0722

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 5 DWG 7

RESULT 4

PT0728

T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0728

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0728

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 4 DWG 6

RESULT 5

PT0724

T-cell receptor beta chain V-D-J region (140-2C) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0724; PT0555
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0724
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-8 <FEE>
 A;Experimental source: newborn thymus, strain BALB/c (clone 140-2C)
 A;Accession: PT0555
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-8 <FE2>
 A;Experimental source: day 18 fetal thymus, strain BALB/c (clone 126-1AL)
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
 |||
 Db 6 DWG 8

RESULT 6

A40753
 aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) - Pyrococcus furiosus (fragment)
 N;Alternate names: glyceraldehyde:ferredoxin oxidoreductase; red tungsten protein (RTP)
 C;Species: Pyrococcus furiosus
 C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1996
 C;Accession: A40753
 R;Mukund, S.; Adams, M.W.W.
 J. Biol. Chem. 266, 14208-14216, 1991
 A;Title: The novel tungsten-iron-sulfur protein of the hyperthermophilic archaeobacterium, Pyrococcus furiosus, is an aldehyde ferredoxin oxidoreductase. Evidence for its participation in a unique glycolytic pathway.
 A;Reference number: A40753; MUID:91317766; PMID:1907273
 A;Accession: A40753
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <MUK>
 C;Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 37.5%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WGR 6
 |||
 Db 5 WGR 7

RESULT 7

PH1344

Ig heavy chain DJ region (clone C100-91A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1344

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoblastic leukemia as evidence for an in utero transforming event.

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1344

A;Molecule type: DNA

A;Residues: 1-10 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWG 5

|||

Db 5 DWG 7

RESULT 8

PH0923

T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0923

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B. J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0923

A;Molecule type: mRNA

A;Residues: 1-10 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WGR 6

|||

Db 4 WGR 6

RESULT 9

I46922

gene Bots protein - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999

C;Accession: I46922
 R;Ellis, S.A.; Braem, K.A.; Morrison, W.I.
 Immunogenetics 37, 49-56, 1992
 A;Title: Transmembrane and cytoplasmic domain sequences demonstrate at least two expressed bovine MHC class I loci.
 A;Reference number: I46921; MUID:93052564; PMID:1428011
 A;Accession: I46922
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-12 <ELL>
 A;Cross-references: GB:S47738; NID:g258999; PIDN:AAB23972.1; PID:g259000
 C;Genetics:
 A;Gene: Bota

Query Match 37.5%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 4 GRI 6

RESULT 10
 PH0928

T-cell receptor beta chain V-D-J region (clone 14) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0928
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0928
 A;Molecule type: mRNA
 A;Residues: 1-13 <GOL>
 A;Experimental source: concanavalin A-activated lymphoblast
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
 |||
 Db 7 DWG 9

RESULT 11
 I46512

troponin - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
 C;Accession: I46512
 R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
 Nature 302, 718-721, 1983

A;Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shotgun sequencing.
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46512
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-15 <PUT>
A;Cross-references: EMBL:V00896; NID:g1734; PIDN:CAA24261.1; PID:g929766
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 13 GRI 15

RESULT 12

JT0610

leukocyte chemoattractant peptide 9 - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Jan-2001

C;Accession: JT0610

R;Murdoch, W.J.; McCormick, R.J.

Biochem. Biophys. Res. Commun. 184, 848-852, 1992

A;Title: Sequence analysis of leukocyte chemoattractant peptides secreted by periovulatory ovine follicles.

A;Reference number: JT0609; MUID:92246975; PMID:1575752

A;Accession: JT0610

A;Molecule type: protein

A;Residues: 1-15 <MUR>

C;Superfamily: unassigned animal peptides

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 9 GRI 11

RESULT 13

S60007

glial hyaluronate-binding protein - human (fragments)

C;Species: Homo sapiens (man)

C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C;Accession: S60007

R;Perides, G.; Asher, R.A.; Lark, M.W.; Lane, W.S.; Robinson, R.A.; Bignami, A.
Biochem. J. 312, 377-384, 1995

A;Title: Glial hyaluronate-binding protein: a product of metalloproteinase digestion of versican?

A;Reference number: S60007; MUID:96103171; PMID:8526845

A;Accession: S60007

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <PER>

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLD 3
|||
Db 7 CLD 9

RESULT 14

I46511
troponin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C;Accession: I46511
R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A;Title: A new troponin T and cDNA clones for 13 different muscle proteins,
found by shotgun sequencing.
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-17 <PUT>
A;Cross-references: EMBL:V00895; NID:g1732; PIDN:CAA24260.1; PID:g929765
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand

Query Match 37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
|||
Db 13 GRI 15

RESULT 15

I67526
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
C;Accession: I67526
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized
mice is not accompanied by somatic mutation of VH genes.
A;Reference number: I53392; MUID:94298870; PMID:8026526
A;Accession: I67526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-17 <RES>
A;Cross-references: GB:S71350; NID:g550038

C;Genetics:
A;Gene: VH7183

Query Match 37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWG 5
|||
Db 12 DWG 14

Search completed: November 13, 2003, 10:39:56
Job time : 8.83333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 09:55:06 ; Search time 4.33333 Seconds
(without alignments)
86.819 Million cell updates/sec

Title: US-09-228-866-8
Perfect score: 8
Sequence: 1 CLDWGRIC 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1246

Minimum DB seq length: 7
Maximum DB seq length: 21

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3	37.5	13	1	TEML_RANTE	P57104 rana tempor
2	3	37.5	16	1	CAT9_FASHE	P80533 fasciola he
3	3	37.5	20	1	CUDP_VERCH	P80406 verticilliu

4	3	37.5	21	1	ATPB_PHYPA	P80658	physcomitre
5	2	25.0	7	1	UF03_MOUSE	P38641	mus musculu
6	2	25.0	8	1	ACI_THUAL	P18691	thunnus alb
7	2	25.0	8	1	AKH_MELML	P25423	melolontha
8	2	25.0	8	1	COXG_RAT	P80430	rattus norv
9	2	25.0	8	1	LCK1_LEUMA	P21140	leucophaea
10	2	25.0	8	1	LCK2_LEUMA	P21141	leucophaea
11	2	25.0	8	1	LCK3_LEUMA	P21142	leucophaea
12	2	25.0	8	1	LCK4_LEUMA	P21143	leucophaea
13	2	25.0	8	1	LCK5_LEUMA	P19987	leucophaea
14	2	25.0	8	1	LCK6_LEUMA	P19988	leucophaea
15	2	25.0	8	1	LCK7_LEUMA	P19989	leucophaea
16	2	25.0	8	1	LCK8_LEUMA	P19990	leucophaea
17	2	25.0	8	1	RT34_BOVIN	P82929	bos taurus
18	2	25.0	9	1	DNF1_LOCFI	P16339	locusta mig
19	2	25.0	9	1	FAR6_MACRS	P83279	macrobrachi
20	2	25.0	9	1	FIBB_ERYPA	P19346	erythrocebu
21	2	25.0	9	1	FIBB_MACFU	P19345	macaca fusc
22	2	25.0	9	1	FIBB_PAPAN	P19344	papio anubi
23	2	25.0	9	1	FIBB_PAPHA	P19343	papio hamad
24	2	25.0	9	1	FIBB_THEGE	P19342	theropithec
25	2	25.0	9	1	IPYR_RHOVI	P82992	rhodopseudo
26	2	25.0	9	1	PGLR_DIAAB	P81179	diaprepes a
27	2	25.0	9	1	RE42_LITRU	P82075	litoria rub
28	2	25.0	9	1	RS10_SERMA	O68936	serratia ma
29	2	25.0	10	1	AKHX_LOCFI	P81626	locusta mig
30	2	25.0	10	1	BPP8_BOTIN	P30426	bothrops in
31	2	25.0	10	1	GON3_PETMA	P30948	petromyzon
32	2	25.0	10	1	HTF1_ROMMI	P18110	romalea mic
33	2	25.0	10	1	HTF2_CARMO	P11385	carausius m
34	2	25.0	10	1	HTF_HELZE	P16353	heliothis z
35	2	25.0	10	1	HTF_NAUCI	P10939	nauphoeta c
36	2	25.0	10	1	HTF_TABAT	P14596	tabanus atr
37	2	25.0	10	1	LABA_JATMU	P13270	jatropha mu
38	2	25.0	10	1	MALE_KLEPN	Q05564	klebsiella
39	2	25.0	10	1	PNEU_HUMAN	P22103	homo sapien
40	2	25.0	10	1	PNEU_RAT	P21996	rattus norv
41	2	25.0	10	1	TKNB_RANRI	P29135	rana ridibu
42	2	25.0	10	1	TPIS_NICPL	P19118	nicotiana p
43	2	25.0	10	1	UPA5_HUMAN	P30091	homo sapien
44	2	25.0	10	1	XYNB_DICB4	P80717	dictyoglomu
45	2	25.0	11	1	ANGT_CRIGE	P09037	crinia geor

ALIGNMENTS

RESULT 1

TEML_RANTE

ID TEML_RANTE STANDARD; PRT; 13 AA.

AC P57104;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Temporin L.

OS Rana temporaria (European common frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog *Rana*
 RT *temporaria*.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
 CC GRAM-POSITIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7
 |||
 Db 10 GRI 12

RESULT 2

CAT9_FASHE

ID CAT9_FASHE STANDARD; PRT; 16 AA.
 AC P80533;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative cathepsin-like enzyme (EC 3.4.22.-) (Newly excysted juvenile
 DE protein 9) (Fragment).
 OS *Fasciola hepatica* (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; *Fasciola*.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95366993; PubMed=7639732;
 RA Tkalcevic J., Ashman K., Meeusen E.;
 RT "*Fasciola hepatica*: rapid identification of newly excysted juvenile
 RT proteins.";
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
 CC STAGE.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR MEROPS; C01.033; -.
 DR InterPro; IPR000169; SHprot_acsite.
 DR PROSITE; PS00139; THIOLESTER_PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOLESTER_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOLESTER_PROTEASE_ASN; PARTIAL.

KW Hydrolase; Thiol protease.

FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1966 MW; 0B7B18FDB1FA541E CRC64;

Query Match 37.5%; Score 3; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LDW 4

|||

Db 6 LDW 8

RESULT 3

CUDP_VERCH

ID CUDP_VERCH STANDARD; PRT; 20 AA.

AC P80406;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cuticle-degrading protease-like protein (EC 3.4.21.-) (Chymoelastase)

DE (Fragment).

OS Verticillium chlamydosporium.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Verticillium.

OX NCBI_TaxID=40265;

RN [1]

RP SEQUENCE.

RC STRAIN=VC10;

RX MEDLINE=95247009; PubMed=7729666;

RA Segers R., Butt T.M., Keen J.N., Kerry B.R., Peberdy J.F.;

RT "The subtilisins of the invertebrate mycopathogens Verticillium

RT chlamydosporium and Metarhizium anisopliae are serologically and

RT functionally related.";

RL FEMS Microbiol. Lett. 126:227-231(1995).

CC -!- FUNCTION: CAPABLE OF BREACHING THE INSECT CUTICLE.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to peptidase family S8.

DR MEROPS; S08.056; -.

DR InterPro; IPR000209; Peptidase_S8.

DR PROSITE; PS00136; SUBTILASE_ASP; PARTIAL.

DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.

DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.

KW Hydrolase; Serine protease.

FT NON_TER 20 20

SQ SEQUENCE 20 AA; 2113 MW; 26744EC2F7729B19 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GRI 7

|||

Db 13 GRI 15

RESULT 4

ATPB_PHYPA

ID ATPB_PHYPA STANDARD; PRT; 21 AA.
AC P80658;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase beta chain (EC 3.6.3.14) (Fragment).
GN ATPB.
OS Physcomitrella patens (Moss).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; Chloroplast; Thylakoid; Membrane; CF(1);
KW Hydrolase; ATP-binding; Hydrogen ion transport.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2298 MW; 9558E4F5AC89D81A CRC64;

Query Match 37.5%; Score 3; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GRI 7
|||
Db 6 GRI 8

RESULT 5

UF03_MOUSE

ID UF03_MOUSE STANDARD; PRT; 7 AA.
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LD 3
 ||
 Db 6 LD 7

RESULT 6

ACI_THUAL

ID ACI_THUAL STANDARD; PRT; 8 AA.
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
 RT muscle."
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR; A31570; A31570.
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WG 5
 ||
 Db 6 WG 7

RESULT 7

AKH_MELML

ID AKH_MELML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
OC Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A58641; A58641.
DR PIR; S15422; S15422.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DW 4
|
|
Db 7 DW 8

RESULT 8

COXG_RAT
ID COXG_RAT STANDARD; PRT; 8 AA.
AC P80430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIb (EC 1.9.3.1) (AED) (Fragment).
GN COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT. THIS PROTEIN MAY BE ONE OF THE
CC HEME-BINDING SUBUNITS OF THE OXIDASE.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIB FAMILY.
DR PIR; S65381; S65381.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LD 3
||
Db 4 LD 5

RESULT 9

LCK1_LEUMA
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;